

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23214	ENU07008	ANI61C6898: 25-45 269..1113	53-72	738-757	LINAP		g136230	283	138	4.00E-32	38	18	"potassium transport protein, high-affinity ; potassium transport protein TRK1, high-affinity - yeast (Saccharomyces cerevisiae) (strain Saccharomyces uvarum) ; (M57508) high-affinity K+ transporter [Saccharomyces uvarum] " (AB014569) KIAA0669 protein [Homo sapiens] (D89340) dipeptidyl peptidase III [Rattus norvegicus] hypothetical 54.1 KD protein in TPS3-IPP2 intergenic region ; hypothetical protein YMR265c - yeast (Saccharomyces cerevisiae) ; (Z49260) unknown [Saccharomyces cerevisiae] (AF052606) chitin synthase 2 [Exophiala dermatitidis] hypothetical 65.9 KD protein C31A2.12 in chromosome I ; hypothetical protein SPAC31A2.12 - fission yeast (Schizosaccharomyces pombe) ; (Z50113) unknown [Schizosaccharomyces pombe] (U78318) chitinase [Entamoeba dispar] (AE000888) malate dehydrogenase [Methanobacterium thermoautotrophicum] (AL022598) hypothetical protein [Schizosaccharomyces pombe] (AF009921) I100 [Rattus norvegicus] enoyl-[acyl-carrier-protein] reductase (NADH) (NADH-dependent enoyl-ACP reductase) (AJ011965) oxidoreductase [Claviceps purpurea]
23215	ENU07009	ANI61C9885: 108-134 1609..1943	108-134	458-479	LINAP		g3327152	79	32	2.7			
23216	ENU07010	ANI61C89:88 7..1411	55-74	481-504	LINAP		g2832906	78	68	5.00E-11	35	18	
23217	ENU07011	ANI61C137:2 484..2939	22-46	450-477	LINAP		g2497213	70	54	0.000000	32	27	03
23218	ENU07012	ANI61C9887: 27-46 4536..4956	27-46	375-398	LINAP		g3548904	270	129	1.00E-29	40	17	
23219	ENU07013	ANI61C9344: 25-44 1183..3128	25-44	761-780	LINAP		g1175406	479	45	0.0007			
23220	ENU07014	ANI61C6320: 53-72 2654..1308	53-72	792-811	LINAP		g1685360	221	48	6.00E-22			
23221	ENU07015	ANI61C1396: 23-42 1125..1834	23-42	578-597	LINAP		g2622314	390	169	2.00E-41	38	69	
23222	ENU07016	ANI61C2287: 22-49 5829..4008	22-49	805-829	LINAP		g3080513	254	75	9.00E-13	26	25	
23223	ENU07017	ANI61C1403: 92-111 1512..1	92-111	723-749	LINAP		g2653779	572	172	2.00E-42	37	37	
23224	ENU07018	ANI61C8897: 36-63 1180..874	36-63	454-479	LINAP		g1169593	77	59	0.000000			
23225	ENU07019	ANI61C9319: 52-71 7975..8612	52-71	582-601	LINAP		g4499843	134	54	0.000001	37	24	

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23226	ENU07020	ANI61C1431: 1307..1908	55-75	446-465	LINAP		g2879805	87	46	0.0002			(AL021813) hypothetical protein [Schizosaccharomyces pombe]
23227	ENU07021	ANI61C8917: 830..1371	22-43	497-521	LINAP		g2330876	275	123	6.00E-28	38	33	[Schizosaccharomyces pombe]
23228	ENU07022	ANI61C9370: 27-49 2680..3096	27-49	411-430	LINAP		g1352686	42	51	0.000006			"protein phosphatase 2C (PP2C) ; phosphoprotein phosphatase (EC 3.1.3.16) 2c, membrane-bound - Paramecium tetraurelia (SGC5) ; (Z36985) PP2C [Paramecium tetraurelia]"
23229	ENU07023	ANI61C2346: 65-84 1..1323	65-84	805-829	LINAP		g3885836	508	82	5.00E-20	28	42	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
23230	ENU07024	ANI61C1412: 22-42 2665..1680	22-42	789-807	LINAP		g117135	584	137	4.00E-60	47	57	cytochrome C oxidase assembly protein COX10 precursor ; COX10 protein precursor - yeast (Saccharomyces cerevisiae) ; (M55566) COX10 [Saccharomyces cerevisiae] ; (Z73528) ORF YPL172c [Saccharomyces cerevisiae]
23231	ENU07025	ANI61C6288: 35-54 2142..1088	35-54	783-802	LINAP		g2237512	577	46	0.0002			(AB004535) hypothetical protein YPR112c [Schizosaccharomyces pombe]
23232	ENU07026	ANI61C6888: 29-49 1..2334	29-49	810-829	LINAP		g1546072	735	126	2.00E-28	29	11	(U68040) polyketide synthase [Cochliobolus heterostrophus]
23233	ENU07027	ANI61C8905: 28-48 1938..1	28-48	765-784	LINAP		g128340	158	46	0.0003			nitrogen assimilation transcription factor NIRA ; nitrate assimilation regulatory protein nirA - Emericella nidulans ; (M68900) NIRA protein [Emericella nidulans]
23234	ENU07028	ANI61C1412: 22-49 3441..3876	22-49	405-425	LINAP		g3165391	151	78	4.00E-14	34	58	(AB014471) compared with Cricetulus griseus SL15 mRNA; GenBank Accession Number U55387 [Mus musculus]
23235	ENU07029	ANI61C8909: 22-42 530..1462	22-42	802-829	LINAP		g539247	840	121	5.00E-38	43	12	SPO14 protein - yeast (Saccharomyces cerevisiae) ; (Z28256) ORF YKR031c [Saccharomyces cerevisiae]
23236	ENU07030	ANI61C6288: 23-42 6978..4884	23-42	805-829	LINAP		g388367	1750	220	7.00E-57	40	38	(L19875) Dur3 [Saccharomyces cerevisiae]

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23237	ENU07031	ANI61C8926: 1015..1	22-47	772-792	LINAP		g122798	85	65	7.00E-10			hemocyanin D chain ; hemocyanin chain d - American tarantula (Eurpelma californica)
23238	ENU07032	ANI61C1439: 26-53 650..1414	26-53	716-735	LINAP		g118571	164	118	6.00E-26			granaticin polyketide synthase putative ketoacyl reductase 1 (ORF5) ; granaticin-producing polyketide synthase chain 5 - Streptomyces violaceoruber ; (X16144) ketoacyl reductase (AA 1-273) [Streptomyces violaceoruber] ; (X16300) ORF 5 (AA 1-272) [Streptomyces violaceoruber] ; (AJ011500) polyketide ketoreductase [Streptomyces violaceoruber] modifier 3 protein (M33) ; modifier-3 protein - mouse ; (X62537) modifier 3 (M33) [Mus musculus] (AF060544) androgen receptor associated protein 54 [Homo sapiens] (AL031518) putative phospholipase [Schizosaccharomyces pombe] hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae) ; (U10400) Ysc84p [Saccharomyces cerevisiae] (AL031856) hypothetical protein [Schizosaccharomyces pombe] IKI3 protein ; probable membrane protein YLR384c - yeast (Saccharomyces cerevisiae) ; (U19104) Iki3p [Saccharomyces cerevisiae] ; (D87841) Iki3p [Saccharomyces cerevisiae]
23239	ENU07033	ANI61C8916: 282..845	24-43	520-539	LINAP		g266545	98	31	5.3			
23240	ENU07034	ANI61C3321: 316..1	102-124	459-478	LINAP		g4530066	73	37	0.08	29	30	
23241	ENU07035	ANI61C9931: 1378..1	24-48	723-749	LINAP		g3560189	372	135	3.00E-31	37	35	
23242	ENU07036	ANI61C322: 92..1337			LINAP		g626598	199	75	4.00E-19	40	42	
23243	ENU07037	ANI61C6894: 1533..2570	22-48	789-815	LINAP		g3738165	310	85	5.00E-23	34	34	
23244	ENU07038	ANI61C2329: 5487..5174			LINAP		g2498477	219	74	4.00E-13	49	7	
23245	ENU07039	ANI61C6906: 1..797	111-131	744-764	LINAP		g3334399	119	50	0.00002	27	28	ubiquitin carboxyl-terminal hydrolase 16 (ubiquitin thiolesterase 16) (ubiquitin-specific processing protease 16) (deubiquitinating enzyme 16) ; probable membrane protein YPL072w - yeast (Saccharomyces cerevisiae) ; (U41849) Lpf12p [Saccharomyces cerevisiae]

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23246	ENU07040	ANI61C9403: 22-41 1344..1768	22-41	455-479	LINAP		g418404	335	159	1.00E-38	55	29	guanosine-diphosphatase (GDPASE) ; guanosine-diphosphatase (EC 3.6.1.42) - yeast (Saccharomyces cerevisiae) ; (L19560) guanosine diphosphatase [Saccharomyces cerevisiae] ; (U18779) Gdalp: guanosine-diphosphatase of Golgi membrane [Saccharomyces cerevisiae]
23247	ENU07041	ANI61C3333: 22-47 3433..4136	22-47	576-595	LINAP		g1685364	233	130	1.00E-29	30	45	(U78320) chitinase [Entamoeba invadens]
23248	ENU07042	ANI61C2366: 29-48 1150..1	29-48	725-749	LINAP		g3282044	1664	510	e-144	86	19	(Y13967) alpha-aminoadipate reductase large subunit [Penicillium chrysogenum]
23249	ENU07043	ANI61C691:8 53-71 84..564	53-71	410-430	LINAP		g544446	43	47	0.00007			membrane transporter D1 ; membrane transport protein (clone D1.SH) - Leishmania donovani ; (M85072) D1 transporter [Leishmania donovani] ; myo-inositol/H symporter [Leishmania donovani]
23250	ENU07044	ANI61C9381: 3456..3877			LINAP		g2706465	157	92	3.00E-18	34	19	(AL021046) positive regulator of camp dependent protein kin ase [Schizosaccharomyces pombe]
23251	ENU07045	ANI61C2373: 38-59 815..203	38-59	567-586	LINAP		g4263825	350	98	3.00E-35	42	16	(AC006067) hypothetical protein [Arabidopsis thaliana]
23252	ENU07046	ANI61C1454: 23-42 668..1	23-42	566-588	LINAP		g2415403	232	109	1.00E-23	32	50	(AF015775) acetylornitine deacetylase [Bacillus subtilis] ; (Z99114) acetylornitine deacetylase [Bacillus subtilis]
23253	ENU07047	ANI61C6226: 69-88 2377..306	69-88	805-823	LINAP		g1084543	546	230	1.00E-59	39	12	FAB1 protein - yeast (Saccharomyces cerevisiae) ; (D50617) FAB1 protein [Saccharomyces cerevisiae]
23254	ENU07048	ANI61C992:7 27-54 69..1308	27-54	488-507	LINAP		g1582765	126	67	8.00E-11	32	29	YFW1 gene [Saccharomyces cerevisiae]

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23255	ENU07049	ANI61C2379: 835..1525			LINAP		g417780	145	50	3.00E-11	35	29	meiosis induction protein kinase IME2/SME1 ; probable protein kinase SME1 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) ; (X53262) protein kinase homologue [Saccharomyces cerevisiae] ; (X85021) SME1 [Saccharomyces cerevisiae] ; (Z49381) ORF YJL106w [Saccharomyces cerevisiae] (AL023592) rna binding protein [Schizosaccharomyces pombe] (Y12709) tealp [Schizosaccharomyces pombe] ; (AL031579) cell polarity protein [Schizosaccharomyces pombe] hypothetical 98.4 KD protein C19G10.07 in chromosome I ; (Z69909) multiple BRCT domain containing protein [Schizosaccharomyces pombe] hypothetical 130.0 KD protein in SNF6-SPO11 intergenic region ; hypothetical protein YHL023c - yeast (Saccharomyces cerevisiae) ; (U11582) No definition line found [Saccharomyces cerevisiae] hypothetical protein YOR049c - yeast (Saccharomyces cerevisiae) ; (Z74957) ORF YOR049c [Saccharomyces cerevisiae] histone H1.1 ; histone H1.1 - Arabidopsis thaliana ; (X62458) Histone H1 [Arabidopsis thaliana] transaldolase ; (L47327) transaldolase [Anabaena variabilis] (Z99531) ubiquitin system protein [Schizosaccharomyces pombe]
23256	ENU07050	ANI61C6348: 23-43 1090..1		784-803	LINAP		g1316059	282	113	2.00E-24	26	21	
23257	ENU07051	ANI61C6908: 28-55 1934..721		803-829	LINAP		g2065436	609	192	3.00E-48	38	21	
23258	ENU07052	ANI61C9404: 22-42 1286..1		717-741	LINAP		g1723501	322	122	4.00E-27	28	29	
23259	ENU07053	ANI61C9946: 121-140 1..1277		804-824	LINAP		g731604	169	71	3.00E-17			
23260	ENU07054	ANI61C1405: 22-41 5270..6129		805-826	LINAP		g2132036	215	78	5.00E-17	33	68	
23261	ENU07055	ANI61C6251: 102-124 358..1		452-479	LINAP		g121902	86	33	1.2			
23262	ENU07056	ANI61C6955: 22-41 540..1014		374-392	LINAP		g1729831	114	64	5.00E-10	33	45	
23263	ENU07057	ANI61C9408: 72-91 2559..1452		806-829	LINAP		g2440180	412	126	2.00E-28	31	8	

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23264	ENU07058	ANI61C3372: 107-127 1.343	107-127	299-321	LINAP		g730745	181	99	1.00E-20	43	9	"osomolarity two-component system protein SLN1 ; SLN1 protein - yeast (Saccharomyces cerevisiae) ; (U01835) Sln1p [Saccharomyces cerevisiae] ; (Z38059) sln1, len: 1220, CAI: 0.13, similar to two component regulatory proteins [Saccharomyces cerevisiae] " hypothetical 37.9 KD protein in STE12-NAM8 intergenic region ; hypothetical protein YHR085w - yeast (Saccharomyces cerevisiae) ; (U10556) Yhr085wp [Saccharomyces cerevisiae] STB2 protein ; SIN3 protein-binding protein STB2 - yeast (Saccharomyces cerevisiae) ; (Z49703) unknown [Saccharomyces cerevisiae] ; (U33438) Stb2p [Saccharomyces cerevisiae] (AL035521) hypothetical protein [Arabidopsis thaliana] (AL034352) hypothetical protein [Schizosaccharomyces pombe] (Z98849) putative dna repair helicase [Schizosaccharomyces pombe] hypothetical 71.9 KD protein in PM140-PAC2 intergenic region ; hypothetical protein YER005w - yeast (Saccharomyces cerevisiae) ; (U18778) Yer005wp [Saccharomyces cerevisiae] (Z98849) putative centromere protein [Schizosaccharomyces pombe] (AB004539) hypothetical 229.9KD protein in NUC1-PRP21 intergenic region [Schizosaccharomyces pombe] (AL034353) probable metabolite transport protein [Schizosaccharomyces pombe]
23265	ENU07059	ANI61C2389: 104-130 436..1	104-130	391-417	LINAP		g731682	143	56	0.000000	26	49	
23266	ENU07060	ANI61C1400: 58-77 7790..8761	58-77	786-805	LINAP		g1711559	258	125	5.00E-28	30	33	
23267	ENU07061	ANI61C3370: 22-49 472..1840	22-49	806-828	LINAP		g4455171	478	160	1.00E-38	36	26	
23268	ENU07062	ANI61C1472: 69-87 2044..1716	69-87	416-435	LINAP		g3925763	229	48	0.000000	36	51	
23269	ENU07063	ANI61C6341: 39-66 1805..2935	39-66	801-821	LINAP		g2370478	1370	354	e-106	74	34	
23270	ENU07064	ANI61C6930: 134-157 4924..4444	134-157	416-435	LINAP		g731435	216	74	3.00E-21	36	22	
23271	ENU07065	ANI61C9421: 65-86 390..1	65-86	457-479	LINAP		g2370479	227	111	2.00E-24	35	25	
23272	ENU07066	ANI61C1483: 33-52 850..202	33-52	579-606	LINAP		g2257560	173	93	1.00E-18	30	11	
23273	ENU07067	ANI61C6334: 22-44 883..2416	22-44	805-824	LINAP		g3925778	835	78	2.00E-29	43	46	

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23274	ENU07068	ANI61C6965: 22-46 508..1471	803-829	803-829	LINAP		g1730664	698	152	1.00E-44	40	72	SMM1 protein ; hypothetical protein YNR015w - yeast (Saccharomyces cerevisiae) ; (Z71630) ORF YNR015w [Saccharomyces cerevisiae] ; (X91816) SMM1 protein [Saccharomyces cerevisiae]
23275	ENU07069	ANI61C9916: 22-44 324..1953	802-829	802-829	LINAP		g1706177	1207	183	1.00E-45	43	27	cutinase transcription factor 1 beta ; (U51672) cutinase transcription factor 1 [Fusarium solani f. sp. pisi]
23276	ENU07070	ANI61C1467: 102-124 1..392	349-368	349-368	LINAP		g3970880	193	101	2.00E-21	45	33	(AB015724) nuclear receptor binding factor-1 [Rattus norvegicus]
23277	ENU07071	ANI61C6366: 41-63 43..918	790-811	790-811	LINAP		g2330868	656	231	5.00E-60	58	88	(Z98603) putative proteosome component [Schizosaccharomyces pombe]
23278	ENU07072	ANI61C6991: 34-53 1151..781	312-330	312-330	LINAP		g4499843	204	45	0.0002	42	25	(AJ011965) oxidoreductase [Claviceps purpurea]
23279	ENU07073	ANI61C9395: 28-47 4754..5371	573-597	573-597	LINAP		g2780359	467	202	2.00E-51	52	34	(AB010110) ascorbate oxidase [Acremonium sp.]
23280	ENU07074	ANI61C237:1 822..2409	525-544	525-544	LINAP		g2634103	208	99	2.00E-20	31	4	(Z99113) polyketide synthase [Bacillus subtilis]
23281	ENU07075	ANI61C9452: 106-133 1..566	522-541	522-541	LINAP		g4502497	158	106	1.00E-22	33	61	chromosome 22 open reading frame 1 ; (U84894) 239AB [Homo sapiens]
23282	ENU07076	ANI61C6338: 22-44 2420..1309	800-819	800-819	LINAP		g2648929	102	38	0.000000			(AE000990) aspartate aminotransferase (aspB-3) [Archaeoglobus fulgidus]
23283	ENU07077	ANI61C146:2 232..745	805-829	805-829	LINAP		g3650387	570	121	7.00E-27	32	16	(AL031743) conserved hypothetical protein [Schizosaccharomyces pombe]
23284	ENU07078	ANI61C3374: 22-46 1098..2512	772-791	772-791	LINAP		g1703456	758	188	4.00E-47	48	24	Cation-transporting ATPase PAT1 ; PAT1 protein - slime mold (Dictyostelium discoideum) ; (X89369) PAT1 protein [Dictyostelium discoideum]
23285	ENU07079	ANI61C7547: 22-44 1306..1	761-780	761-780	LINAP		g3337389	1305	380	e-105	67	23	(AC004682) pre-mRNA splicing factor (PRP16)(K1AA0224) [Homo sapiens]
23286	ENU07080	ANI61C9916: 22-41 4011..5218	808-829	808-829	LINAP		g461830	575	104	8.00E-22	39	33	"carboxypeptidase S1 ; carboxypeptidase S1 - Penicillium janthinellum ; carboxypeptidase S1, CPD-S1 [Penicillium janthinellum, Peptide, 423 aa] ; carboxypeptidase S1 [Penicillium janthinellum] "

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23287	ENU07081	ANI61C3345: 1879..983	22-44	808-827	LINAP		g3319757	99	45	0.0007	24	27	(AL031035) putative ATP/GTP-binding protein [Streptomyces coelicolor]
23288	ENU07082	ANI61C6996: 22-46	22-46	456-483	LINAP		g3978134	312	64	7.00E-30	55	13	(U65409) Sla2p [Yarrowia lipolytica]
23289	ENU07083	ANI61C3379: 22-44	22-44	372-399	LINAP		g3925755	225	106	1.00E-22	40	30	(AL034352) putative phosphodiesterase-nucleotide pyrophosphatase precursor [Schizosaccharomyces pombe]
23290	ENU07084	ANI61C239:1..917			LINAP		g3219911	762	250	7.00E-66	54	32	putative kinesin-like protein C2F12.13; (Z97211) kinesin-like protein [Schizosaccharomyces pombe]
23291	ENU07085	ANI61C6990: 44-63	44-63	554-579	LINAP		g1352938	294	127	9.00E-29	37	60	hypothetical 39.7 KD protein in HOM6-PMT4 intergenic region; hypothetical protein YJR142w - yeast (Saccharomyces cerevisiae); (Z49642) ORF YJR142w [Saccharomyces cerevisiae]
23292	ENU07086	ANI61C7552: 23-48	23-48	693-715	LINAP		g2648302	334	171	4.00E-42	50	83	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpcE-2) [Archaeoglobus fulgidus]"
23293	ENU07087	ANI61C9970: 22-48	22-48	465-492	LINAP		g1077378	114	44	0.0007			probable membrane protein YLR222c - yeast (Saccharomyces cerevisiae); (U19027) Ylr222cp [Saccharomyces cerevisiae]
23294	ENU07088	ANI61C3355: 1..522			LINAP		g2131504	282	106	1.00E-22	40	27	hypothetical protein YDR456w - yeast (Saccharomyces cerevisiae); (U33007) Ydr456wp; CAI: 0.16 [Saccharomyces cerevisiae]
23295	ENU07089	ANI61C2400: 53-72	53-72	803-822	LINAP		g2911284	478	90	3.00E-33	47	56	(U97681) putative splicing factor [Schizosaccharomyces pombe]; (AL035675) putative splicing factor. [Schizosaccharomyces pombe]
23296	ENU07090	ANI61C6338: 40-60	40-60	796-815	LINAP		g2330697	240	88	4.00E-23			(Z98529) mating and morphogenesis protein Scd1p. [Schizosaccharomyces pombe]

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23297	ENU07091	ANI61C1504: 27-45 508..1	27-45	382-404	LINAP		g1174862	210	67	3.00E-21	35	33	putative ubiquitin carboxyl-terminal hydrolase C13A11.04C (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme) ; (Z54096) unknown [Schizosaccharomyces pombe] (Z97341) heat shock protein 110 homolog [Arabidopsis thaliana] phosphate transporter - Glomus versiforme ; (U38650) phosphate transporter [Glomus versiforme] ; phosphate transporter [Glomus versiforme]
23298	ENU07092	ANI61C6368: 22-49 3857..3370	22-49	287-306	LINAP		g2245021	125	82	3.00E-15	30	57	
23299	ENU07093	ANI61C3343: 22-49 3736..2779	22-49	807-829	LINAP		g2147899	609	132	2.00E-30	40	47	
23300	ENU07094	ANI61C6335: 66-85 3430..4017	66-85	519-538	LINAP		g725498	72	36	0.29			(U14651) protein VI precursor [Human adenovirus type 40]
23301	ENU07095	ANI61C7006: 59-78 594..1277	59-78	556-575	LINAP		g3258637	82	71	1.00E-11			(AF041050) 4-coumarate:CoA ligase [Populus tremuloides]
23302	ENU07096	ANI61C6335: 163-182 7599..8160	163-182	384-403	LINAP		g2132853	93	48	0.00006	40	52	probable membrane protein YOL146w - yeast [Saccharomyces cerevisiae] ; (Z48239) orf6 [Saccharomyces cerevisiae] ; (Z74888) ORF YOL146w [Saccharomyces cerevisiae]
23303	ENU07097	ANI61C7575: 66-86 419..1	66-86	434-453	LINAP		g3114719	131	46	2.00E-12	34	9	[Saccharomyces cerevisiae] (Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
23304	ENU07098	ANI61C9442: 22-49 4191..3548	22-49	602-623	LINAP		g2827571	149	63	4.00E-10	30	54	(AL021646) hypothetical protein Rv3161c [Mycobacterium tuberculosis]
23305	ENU07099	ANI61C3385: 1126..1478			LINAP		g2135769	61	44	0.000000	30	10	"multidrug resistance protein, canalicular - human ; (X96395) canalicular multidrug resistance protein [Homo sapiens] "
23306	ENU07100	ANI61C2418: 1..3138			LINAP		g3136094	5014	415	e-135	96	23	(AF032987) spindle assembly checkpoint protein SLDA [Emmericella nidulans]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23307	ENU07101	ANI61C1519: 1..384	102-127	339-363	LINAP		g3874095	126	57	0.000000	04		(Z49908) cDNA EST EMBL:D67930 comes from this gene; cDNA EST EMBL:D27476 comes from this gene; cDNA EST yk317d5.5 comes from this gene; cDNA EST yk443d4.5 comes from this gene; cDNA ES...; (Z81573) cDNA EST EMBL:D67930 comes from this gene; cDNA EST EMBL:D27476 comes from this gene; cDNA EST EMBL:D27475 comes from this gene; cDNA EST yk317d5.5 comes from this gene; cDNA EST yk443d4.5 comes from this gene; cDNA ES...; (Z99268) cDNA EST EMBL:D67930 comes from this gene; cDNA EST EMBL:D27476 comes from this gene; cDNA EST EMBL:D27475 comes from this gene; cDNA EST yk317d5.5 comes from this gene; cDNA EST yk443d4.5 comes from this gene; cDNA ES...
23308	ENU07102	ANI61C6992: 412..1	45-72	457-479	LINAP		g2133035	345	113	3.00E-29	48	30	probable membrane protein YPR157w - yeast (Saccharomyces cerevisiae); (U28371) P9584.4 gene product [Saccharomyces cerevisiae] neutrophil cytosolic factor 2; p67phox; 67K neutrophil oxidase factor - human; (M32011) neutrophil oxidase factor [Homo sapiens] elongation factor 1-gamma (EF-1-gamma); translation elongation factor eEF-1 gamma chain - brine shrimp; (M28020) elongation factor 1-gamma [Artemia sp.]
23309	ENU07103	ANI61C7532: 1..595	68-94	550-572	LINAP		g4557787	172	74	3.00E-19	31	35	
23310	ENU07104	ANI61C9963: 920..596	22-48	457-479	LINAP		g119164	149	54	0.000000	44	17	
23311	ENU07105	ANI61C3351: 6114..7195	22-42	785-809	LINAP		g2462679	110	75	9.00E-13	24	29	(Z99568) putative regulatory protein; zinc finger [Schizosaccharomyces pombe]

Seq num	Seq id	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23312	ENU07106	Contig source ANI61C2433: 22-43 501..1	332-359	LINAP		g396376	247	119	1.00E-26	38	18	(U00006) glycerol-3-phosphate acyltransferase [Escherichia coli]
23313	ENU07107	ANI61C1524: 22-49 3022..2112	807-827	LINAP		g3218397	466	111	6.00E-24	38	34	(AL023860) hypothetical protein [Schizosaccharomyces pombe]
23314	ENU07108	ANI61C7026: 65..750		LINAP		g2660670	174	90	1.00E-17	30	23	(AC002342) putative Cu+-transporting ATPase [Arabidopsis thaliana]
23315	ENU07109	ANI61C7532: 38-57 2776..3178	453-479	LINAP		g1717966	88	46	0.0001	23	40	UFE1 protein; UFE1 protein - yeast (Saccharomyces cerevisiae); (L15081) UFE1 gene product [Saccharomyces cerevisiae]; (U53416) Ufe1p [Saccharomyces cerevisiae]; (Z74983) ORF YOR075w [Saccharomyces cerevisiae]; (Z70678) YOR29-26 [Saccharomyces cerevisiae]
23316	ENU07110	ANI61C9485: 42-60 2172..2716	487-511	LINAP		g2500938	314	74	2.00E-26	44	28	myo-inositol transporter 1; (X98622) myo-inositol transporter [Schizosaccharomyces pombe]
23317	ENU07111	ANI61C339:1 22-43 110..421	607-629	LINAP		g3153821	20	41	0.006			(AF062655) plenty-of-prolines-101; POP101; SH3-philoprotein [Mus musculus]
23318	ENU07112	ANI61C2444: 22-48 1043..700	430-457	LINAP		g1805251	152	85	3.00E-16	32	28	(U58946) transposase [Aspergillus awamori]
23319	ENU07113	ANI61C6363: 29-56 4145..5494	747-774	LINAP		g2388895	350	61	0.000000			(Z98981) hypothetical protein [Schizosaccharomyces pombe]
23320	ENU07114	ANI61C9995: 39-58 79..840	717-741	LINAP		g4104400	130	38	0.11			(AF035401) exocellobiohydrolase precursor [Piromyces rhizinflata]
23321	ENU07115	ANI61C244:2 55-79 292..1664	587-606	LINAP		g4200325	160	76	3.00E-13			(Z98885) dJ522J7.2 (Peregrin (BR140) like protein) [Homo sapiens]
23322	ENU07116	ANI61C1494: 4073..4386		LINAP		g562121	106	62	0.000000	39	16	(U16137) Mvp1p [Saccharomyces cerevisiae]
23323	ENU07117	ANI61C6387: 71-90 695..281	457-476	LINAP		g3288594	198	74	3.00E-18	44	11	(AJ006340) 26S proteasome subunit p112 [Rattus norvegicus]
23324	ENU07118	ANI61C1547: 22-47 572..260	447-466	LINAP		g1175451	131	80	1.00E-14	36	8	hypothetical protein C22F3.14C in chromosome 1; hypothetical protein SPAC22F3.14c - fission yeast (Schizosaccharomyces pombe); (Z54285) unknown [Schizosaccharomyces pombe]

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Seq num	Seq id	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23325	ENU07119	Contig source ANI61C7576: 1737..2047		LINAP		g1078614	212	96	3.00E-20	47	21	stearoyl-CoA desaturase (EC 1.14.99.5) - Ajellomyces capsulata ; (X85962) delta-9 fatty acid desaturase [Ajellomyces capsulatus] (AB010438) organic-cation transporter like 3 [Homo sapiens] putative tartrate transporter ; (U32375) membrane protein [Agrobacterium vitis]
23326	ENU07120	ANI61C339:2 41-59 465..2107	456-479	LINAP		g4586315	104	57	0.000000 06	28	29	
23327	ENU07121	ANI61C9972: 22-43 1208..2292	790-809	LINAP		g4033481	224	110	1.00E-23	33	53	
23328	ENU07122	ANI61C7593: 27-46 972..357	379-397	LINAP		g3136052	235	62	0.000000 004	40	34	(AL023592) acetamidase [Schizosaccharomyces pombe]
23329	ENU07123	ANI61C9992: 32-54 1870..1	779-803	LINAP		g3184062	240	59	7.00E-19	31	16	(AL023776) hypothetical protein [Schizosaccharomyces pombe]
23330	ENU07124	ANI61C2437: 1456..399		LINAP		g3406059	603	124	8.00E-55	52	61	(AF017646) TFIIF subunit p47 [Schizosaccharomyces pombe] ; (AL031525) tfiif subunit p47. [Schizosaccharomyces pombe]
23331	ENU07125	ANI61C7578: 30-49 1121..2101	782-801	LINAP		g3024604	169	46	0.0004	26	23	suppressor protein SEF1 ; (U92898) suppressor protein [Kluyveromyces lactis]
23332	ENU07126	ANI61S1068: 104-130 439..1	373-395	LINAP		g2619050	97	56	0.000000 1	27	55	(AF027868) YocH [Bacillus subtilis] ; (Z99114) similar to cell wall-binding protein [Bacillus subtilis]
23333	ENU07127	ANI61C3399: 97-119 2562..1	708-731	LINAP		g2147662	793	103	1.00E-21	27	12	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium ; (D83643) polyketide synthase [Colletotrichum lagenarium] (Z99532) putative integral membrane protein [Schizosaccharomyces pombe]
23334	ENU07128	ANI61C2439: 62-82 318..1	456-476	LINAP		g2440206	307	136	8.00E-32	39	21	
23335	ENU07129	ANI61C6408: 40-59 2484..889	809-829	LINAP		g3135990	1070	171	4.00E-42	49	46	protein [Schizosaccharomyces pombe] (AL023589) membrane transporter [Schizosaccharomyces pombe] (M36482) SNF5 protein [Saccharomyces cerevisiae]
23336	ENU07130	ANI61C7586: 46-65 1171..1	613-630	LINAP		g172638	430	153	1.00E-36	42	21	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23337	ENU07131	ANI61C9493: 35-62 3165..373	715-739	715-739	LINAP		g548817	2756	333	1.00E-90	59	15	DNA-directed RNA polymerase II largest subunit (RNA polymerase II subunit 1) ; DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain - fission yeast (Schizosaccharomyces pombe) ; (X56564) RNA polymerase II large subunit [Schizosaccharomyces pombe] (AL035076) putative allantoate permease [Schizosaccharomyces pombe]
23338	ENU07132	ANI61C3414: 38-60 1630..2327	567-586	567-586	LINAP		g4107287	184	80	1.00E-23	41	32	(AJ009555) hypothetical protein [Arabidopsis thaliana] (AL031349) conserved hypothetical protein [Schizosaccharomyces pombe] (Z70751) similar to 4-coumarate-CoA ligase; cDNA EST EMBL:C07240 comes from this gene; cDNA EST EMBL:C08540 comes from this gene [Caenorhabditis elegans] hypothetical 210.4 KD protein in GUT1-RIM1 intergenic region ; hypothetical protein YHL030w - yeast (Saccharomyces cerevisiae) ; (U11583) YHL030w gene product [Saccharomyces cerevisiae] (AF093142) aconitase [Aspergillus terreus]
23339	ENU07133	ANI61C243:2 51-70 14..1076	809-828	809-828	LINAP		g4200122	462	119	4.00E-35	48	100	SMP2 protein ; SMP2 protein - yeast (Saccharomyces cerevisiae) ; (D01095) Smp2p [Saccharomyces cerevisiae] ; (Z49705) Smp2p [Saccharomyces cerevisiae] ; SMP2 gene [Saccharomyces cerevisiae] (L40632) ankyrin 3 [Mus musculus]
23340	ENU07134	ANI61C9478: 44-63 721..1	644-663	644-663	LINAP		g3451474	753	300	9.00E-81	62	38	
23341	ENU07135	ANI61C2443: 118-140 452..1	460-479	460-479	LINAP		g3875727	50	58	0.000000			
23342	ENU07136	ANI61C7019: 22-42 2157..358	785-812	785-812	LINAP		g731610	336	74	1.00E-12			
23343	ENU07137	ANI61C3440: 42-69 402..795	362-381	362-381	LINAP		g3661614	604	228	3.00E-59	84	17	
23344	ENU07138	ANI61C2443: 24-46 3603..2148	798-821	798-821	LINAP		g417782	773	212	5.00E-74	56	30	
23345	ENU07139	ANI61C9482: 24-46 3304..3985	635-659	635-659	LINAP		g710551	182	84	1.00E-15			
23346	ENU07140	ANI61S138:9 67..501			LINAP		76					29	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23347	ENU07141	ANI61C342:2 543..874	22-44	809-829	LINAP		g4309732	141	33	2.3			(AC006439) hypothetical protein [Arabidopsis thaliana]
23348	ENU07142	ANI61C6406: 1516..4364	71-90	762-780	LINAP		g3298562	1004	61	0.000000			(U91543) zinc-finger helicase [Homo sapiens]
23349	ENU07143	ANI61C7015: 4595..3707	22-47	781-800	LINAP		g3133109	463	141	8.00E-33	33	38	(AL023354) fork head protein type transcription factor [Schizosaccharomyces pombe]
23350	ENU07144	ANI61S1513: 1..553	168-187	331-350	LINAP		g1351702	67	67	1.00E-10			hypothetical 61.1 KD protein C11D3.05 in chromosome I; (Z68166) unknown [Schizosaccharomyces pombe]
23351	ENU07145	ANI61C3439: 888..1	36-55	800-825	LINAP		g4107480	332	69	9.00E-27	47	39	(AL035085) putative mitochondrial carrier protein [Schizosaccharomyces pombe]
23352	ENU07146	ANI61C6426: 311..1385			LINAP		g2073105	546	185	4.00E-46	42	38	(AB003310) chitin synthase regulatory factor [Candida albicans]
23353	ENU07147	ANI61C7062: 574..267	27-54	263-287	LINAP		g4557813	65	52	0.000001	30	11	"phosphatidylinositol polyphosphate 5-phosphatase, isoform a; (U57627) ocr1l [Homo sapiens]"
23354	ENU07148	ANI61C7611: 2352..1355	155-179	681-700	LINAP		g4049510	170	86	3.00E-16	29	49	(AL034563) putative polyA-binding protein. [Schizosaccharomyces pombe]
23355	ENU07149	ANI61S187:3 02..898			LINAP		g2493724	199	79	2.00E-14	44	32	"citrate synthase, mitochondrial precursor; (AB001565) citrate synthase [Candida tropicalis]"
23356	ENU07150	ANI61C2463: 425..1	146-165	455-479	LINAP		g2842469	360	157	6.00E-38	46	21	(AL021747) hypothetical protein [Schizosaccharomyces pombe]
23357	ENU07151	ANI61C6416: 4247..4853	38-57	558-585	LINAP		g1857082	62	39	0.023			(U59915) Noc1p [Schizosaccharomyces pombe]; (Z99568) noc1p. [Schizosaccharomyces pombe]
23358	ENU07152	ANI61C7029: 4146..2624	71-90	806-825	LINAP		g1169238	935	133	4.00E-63	56	51	"glutamate decarboxylase (GAD); glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding - garden petunia; (L16797) glutamate decarboxylase [Petunia hybrida]; (L16977) glutamate decarboxylase [Petunia hybrida]"
23359	ENU07153	ANI61S2140: 234..722			LINAP		g4539416	82	67	1.00E-10	37	20	(AL049171) l-aminocyclopropane-l-carboxylate synthase-like protein [Arabidopsis thaliana]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23360	ENU07154	ANI61C2464: 434..1	102-120	415-434	LINAP		g479416	189	87	1.00E-16	30	24	kinasin light chain isoform 3 - sea urchin (Strongylocentrotus purpuratus)
23361	ENU07155	ANI61C6433: 3153..2606	197-219	498-516	LINAP		g4033486	200	101	3.00E-21			putative tartrate transporter ; (U25634) putative tartrate transporter; inducible by tartrate; Method: conceptual translation supplied by author. [Agrobacterium vitis] ; tuB gene [Agrobacterium vitis]
23362	ENU07156	ANI61C955:9 21..1	44-68	722-749	LINAP		g4481951	734	148	3.00E-74	59	10	(AL035637) putative alpha-glucan synthase [Schizosaccharomyces pombe]
23363	ENU07157	ANI61C2468: 1656..2169	22-48	470-493	LINAP		g2132222	117	48	0.00004	30	29	hypothetical protein YPL181w - yeast (Saccharomyces cerevisiae) ; (Z73538) ORF YPL181w [Saccharomyces cerevisiae]
23364	ENU07158	ANI61C6422: 4382..4079	22-49	443-462	LINAP		g4263745	38	47	0.00009			"(AC004912) similar to CR16, SH3 domain binding protein; similar to 2205340A (PID:g1587070) [Homo sapiens]"
23365	ENU07159	ANI61C3420: 4161..4662	22-45	373-392	LINAP		g539323	323	143	1.00E-33	42	21	mitochondrial intermediate peptidase (EC 3.4.24.-) precursor - yeast (Saccharomyces cerevisiae) ; (Z28134) ORF YKL134c [Saccharomyces cerevisiae]
23366	ENU07160	ANI61S2566: 144..575	28-49	274-300	LINAP		g417049	110	79	2.00E-14	36	20	Gephyrin (putative glycine receptor-tubulin linker protein) ; gephyrin - rat ; (X66366) Gephyrin [Rattus norvegicus]
23367	ENU07161	ANI61C7048: 2867..3715	24-46	715-739	LINAP		g1351661	128	82	4.00E-15	29	37	hypothetical 60.7 KD protein C30D11.08C in chromosome I ; hypothetical protein SPAC30D11.08c - fission yeast (Schizosaccharomyces pombe) ; (Z67961) PHD finger protein [Schizosaccharomyces pombe]

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23368	ENU07162	ANI61C7624: 423..1	29-56	453-479	LINAP		g549758	67	50	0.00001			"FERRIC reductase transmembrane component 2 precursor ; ferric reductase FRE2 precursor - yeast (Saccharomyces cerevisiae) ; (X75950) ORF5, F711 [Saccharomyces cerevisiae] ; (Z28220) ORF YKL220c [Saccharomyces cerevisiae] ; ORF 5 [Saccharomyces cerevisiae] "
23369	ENU07163	ANI61S269:1..706	122-141	584-601	LINAP		g1679757	362	152	9.00E-40	39	30	(U77605) two-component histidine kinase CHK-1 [Glomerella cingulata] ; (U77606) two-component histidine kinase CHK-1 [Glomerella cingulata] (Z37980) hypothetical 4-hydroxyphenylacetate permease [Escherichia coli] (M18209) transcription factor S-II [Mus musculus] (L77234) glycine rich protein [Neurospora crassa] (M80368) pathway-specific regulatory protein [Neurospora crassa] chromosome scaffold protein sudA - Emericella nidulans ; (U40146) chromosome scaffold protein [Emericella nidulans] maltose permease MAL3T (maltose transport protein MAL3T) ; maltose transport protein MAL3T - yeast (Saccharomyces cerevisiae) ; (Z36167) ORF YBR298c [Saccharomyces cerevisiae]
23370	ENU07164	ANI61C3451: 2042..1199	36-63	792-819	LINAP		g757832	235	55	2.00E-15			
23371	ENU07165	ANI61C2468: 2660..3004	22-48	454-479	LINAP		g201937	81	74	6.00E-13	33	58	
23372	ENU07166	ANI61C7056: 2961..992	22-45	807-826	LINAP		g1261823	944	122	4.00E-27	36	28	
23373	ENU07167	ANI61C9538: 2083..1066	26-53	801-820	LINAP		g168849	144	56	5.00E-11	29	22	
23374	ENU07168	ANI61S298:1..458	149-168	291-318	LINAP		g2133266	311	97	8.00E-20	68	11	
23375	ENU07169	ANI61C248:1..359..1	25-45	757-780	LINAP		g585446	310	88	7.00E-17	23	45	
23376	ENU07170	ANI61C7021: 1..5469	22-43	801-828	LINAP		g2342601	2446	157	3.00E-44	38	5	(X89442) peptide synthetase [Metarhizium anisopliae]
23377	ENU07171	ANI61S3228: 569..243	136-161	276-294	LINAP		g4455254	181	94	4.00E-19	74	16	(AL035523) putative protein [Arabidopsis thaliana]

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23378	ENU07172	ANI61C9548: 72-91 2731..2342	72-91	301-320	LINAP	Database Hit	g586300	275	125	1.00E-28	44	34	hypothetical 44.4 KD protein in CDC28-ARL1 intergenic region ; SUR1 protein homolog YBR161w - yeast (Saccharomyces cerevisiae) ; (X80224) YBR1212 [Saccharomyces cerevisiae] ; (Z36030) ORF YBR161w [Saccharomyces cerevisiae] (U78597) kinesin light chain [Plectonema boryanum] (AJ010981) putative transposase [Talaromyces stipitatus] conidial green pigment synthase ; probable polyketide synthase - Emericella nidulans ; (X65866) putative polyketide or fatty acid synthase [Emericella nidulans] ; wA gene [Emericella nidulans] SIS2 protein (halotolerance protein HAL3) ; hal3 protein - yeast (Candida tropicalis) ; (X88900) hal3 [Candida tropicalis] lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] (Z99163) hypothetical protein [Schizosaccharomyces pombe] (Z681119) cDNA EST EMBL:Z14951 comes from this gene; cDNA EST EMBL:T00215 comes from this gene; cDNA EST EMBL:D71583 comes from this gene; cDNA EST EMBL:D74238 comes from this gene; cDNA EST yk376f7.3 comes from this gene; cDNA ...
23379	ENU07173	ANI61S3294: 134-153 1..457	134-153	290-312	LINAP	Database Hit	g2645229	217	89	2.00E-17	36	31	
23380	ENU07174	ANI61C2501: 143-169 1..479	143-169	414-441	LINAP	Database Hit	g3646479	198	94	7.00E-19	32	94	
23381	ENU07175	ANI61C7017: 26-45 1088..1	26-45	722-749	LINAP	Database Hit	g549443	569	214	7.00E-55	39	14	
23382	ENU07176	ANI61S3549: 615..290			LINAP	Database Hit	g2498915	89	56	0.000000	33	19	
23383	ENU07177	ANI61C3502: 47-66 278..991	47-66	669-692	LINAP	Database Hit	g125935	248	112	2.00E-24	31	40	
23384	ENU07178	ANI61C252:1 22-48 513..953	22-48	519-538	LINAP	Database Hit	g2408040	116	46	0.000000	29	70	
23385	ENU07179	ANI61C7653: 22-46 750..401	22-46	433-452	LINAP	Database Hit	g3879884	138	33	1.4	5		

Gene Description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23386	ENU07180	ANI61C9555: 1733..899	72-91	793-814	LINAP		g548976	101	49	0.00004	21	54	suppressor protein SRP40 ; SRP40 protein - yeast (Saccharomyces cerevisiae) ; (X73541) ORF YKR412 [Saccharomyces cerevisiae] ; (Z28317) ORF YKR092c [Saccharomyces cerevisiae]
23387	ENU07181	ANI61S3624: 1..392	47-66	301-323	LINAP		g2687633	61	43	0.00006	44	18	(AF035756) 2-dehydro-3-deoxyphosphoheptonate aldolase; phospho-2-dehydro-3-deoxyheptonate aldolase [Streptomyces sp.] (U28943) similar to ribitol dehydrogenase [Caenorhabditis elegans]
23388	ENU07182	ANI61C2550: 1249..1549	51-70	459-478	LINAP		g861340	69	46	0.0002			(AL049559) conserved hypothetical protein [Schizosaccharomyces pombe] (D87895) chitinase [Emencella nidulans]
23389	ENU07183	ANI61C7020: 1296..2568	22-48	804-829	LINAP		g4581524	695	260	8.00E-69	47	48	(AF001304) protease 1 [Pneumocystis carinii f. sp. carinii]
23390	ENU07184	ANI61C7660: 1990..1287	114-131	661-682	LINAP		g4063766	102	41	0.008			putative tartrate transporter ; (U25634) putative tartrate transporter; inducible by tartrate; Method: conceptual translation supplied by author.
23391	ENU07185	ANI61S3795: 343..1	122-149	259-280	LINAP		g2327061	181	90	9.00E-18	44	12	[Agrobacterium vitis] ; tuB gene [Agrobacterium vitis]
23392	ENU07186	ANI61C7664: 1..735	30-49	692-714	LINAP		g4033486	225	108	6.00E-23			(AF052586) beta-ketoacyl reductase [Pseudomonas aeruginosa]
23393	ENU07187	ANI61S4106: 416..1	138-158	299-318	LINAP		g2970667	157	81	6.00E-15	28	48	hypothetical 216.3 KD protein R06F6.8 in chromosome II ; (Z46794) cDNA EST EMBL: T01654 comes from this gene; cDNA EST EMBL: D32326 comes from this gene; cDNA EST
23394	ENU07188	ANI61C9570: 3084..1369	22-47	798-817	LINAP		g2496987	140	96	4.00E-19	35	8	EMBL: D32810 comes from this gene; cDNA EST EMBL: D34680 comes from this gene; cDNA EST EMBL: D35556 comes from this gene; cDN...

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23395	ENU07189	ANI61S4269: 1..380	87-106	229-248	LINAP		g730742	159	83	6.00E-16	32	10	SIP3 protein ; SIP3 protein - yeast (Saccharomyces cerevisiae) ; (U03376)
23396	ENU07190	ANI61C2478: 72-91 2192..1830	72-91	452-471	LINAP		g2501705	125	87	1.00E-16			Sip3p [Saccharomyces cerevisiae] ; (X96722) ORF N0844 [Saccharomyces cerevisiae] ; (Z71533) ORF YNL257c [Saccharomyces cerevisiae] zinc finger protein GLI4 (neural specific DNA binding protein XGLI4) (XGLI-4) ; (U42462) neural specific DNA binding protein [Xenopus laevis] A-agglutinin attachment subunit precursor ; a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae) ; (M60590) a-agglutinin core subunit [Saccharomyces cerevisiae] ; (Z71659) ORF YNR044w [Saccharomyces cerevisiae] (Z99165) hypothetical protein [Schizosaccharomyces pombe] (U59303) glucoamylase precursor [Aspergillus awamori] (U75445) alpha-amylase [Bacillus sp. MK 716] HC-toxin synthetase (HTS) ; (M98024) HC-toxin synthetase [Cochliobolus carbonum] (Z98741) oxidoreductase [Mycobacterium leprae] hypothetical 73.1 KD protein C3H1.09C in chromosome I ; (Z68144) major facilitator superfamily protein [Schizosaccharomyces pombe] (Z50144) kynurenine/alpha-aminoadipate aminotransferase [Rattus norvegicus] "(U66480) xylan beta-1,4-xylosidase [Bacillus subtilis] ; (Z99113) xylan beta-1,4-xylosidase [Bacillus subtilis] "
23397	ENU07191	ANI61C7092: 24-43 925..89	24-43	796-816	LINAP		g416592	84	46	0.0002			
23398	ENU07192	ANI61C9586: 46-65 1358..1838	46-65	410-431	LINAP		g2408062	189	87	1.00E-16	45	20	
23399	ENU07193	ANI61C2555: 22-45 2559..2969	22-45	428-447	LINAP		g1389841	380	122	2.00E-27	50	26	
23400	ENU07194	ANI61S4557: 32-51 221..599	32-51	328-347	LINAP		g1667474	69	61	0.000000			
23401	ENU07195	ANI61S4598: 61-85 480..1	61-85	443-469	LINAP		g462367	212	106	1.00E-22	33	3	
23402	ENU07196	ANI61C347:3 118-137 07..1	118-137	443-462	LINAP		g2342610	88	43	0.000000	32	21	
23403	ENU07197	ANI61S4611: 33-53 1..391	33-53	334-353	LINAP		g1351692	194	92	2.00E-18	37	19	
23404	ENU07198	ANI61C2593: 56-75 1288..568	56-75	667-689	LINAP		g1050752	110	60	6.00E-12			
23405	ENU07199	ANI61C3538: 48-75 1607..354	48-75	810-829	LINAP		g1750122	303	57	1.00E-11			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23413	ENU07207	ANI61C355:3 085..1963	22-45	807-828	LINAP		g2136300	492	34	1			transcription factor NFATx - human ; (U14510) NFATx [Homo sapiens]
23414	ENU07208	ANI61C7071: 3980..6963			LINAP		g1799570	680	105	2.00E-27	39	19	(D87671) TIP120 [Rattus norvegicus]
23415	ENU07209	ANI61S577:1. 314	62-81	249-272	LINAP		g2225966	112	53	0.000000	29	27	(Z97193) hypothetical protein Rv1894c [Mycobacterium tuberculosis]
23416	ENU07210	ANI61C7706: 1007..584	30-51	454-476	LINAP		g126643	63	55	0.000000			Aminoacidipate-semialdehyde dehydrogenase large subunit (alpha-aminoacidipate reductase) (alpha-AR) ; L-aminoacidipate-semialdehyde dehydrogenase (EC 1.2.1.31) - yeast (Saccharomyces cerevisiae) ; (M36287) alpha-aminoacidipate reductase (LYS2; EC 1.2.1.31) [Saccharomyces cerevisiae] ; (X78993) alpha-aminoacidipate reductase [Saccharomyces cerevisiae] ; (Z35984) ORF YBR115c [Saccharomyces cerevisiae] ; (AD001531) alpha-aminoacidipate reductase [Cloning vector pGR8]
23417	ENU07211	ANI61C3550: 3384..4143	22-44	691-710	LINAP		g3876027	147	92	5.00E-18	34	16	(Z78062) cDNA EST EMBL:D34090 comes from this gene; cDNA EST EMBL:D37114 comes from this gene; cDNA EST EMBL:D64639 comes from this gene; cDNA EST EMBL:D67728 comes from this gene; cDNA EST EMBL:C12617 comes from this gene; cDN...
23418	ENU07212	ANI61S77:33 8..1			LINAP		g2492657	336	149	1.00E-35	62	8	putative sterigmatocystin biosynthesis fatty acid synthase alpha subunit ; (U34740) putative fatty acid synthase alpha [Emmericella nidulans]

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23419	ENU07213	ANI61C7674: 29-52 3380..2309	5 pos	802-829	LINAP	g1730824	363	60	5.00E-10	40	42		hypothetical 56.6 KD protein in URE2-SSU72 intergenic region ; hypothetical protein YNL223w - yeast (Saccharomyces cerevisiae) ; (Z69381) N1274 [Saccharomyces cerevisiae] ; (Z71499) ORF YNL223w [Saccharomyces cerevisiae]
23420	ENU07214	ANI61S79:1..595			LINAP	g127736	183	94	1.00E-18	30	12		myosin-2 isoform ; myosin myo2 - yeast (Saccharomyces cerevisiae) ; (M35532) myosin 1 isoform (myo2) [Saccharomyces cerevisiae] ; (Z75234) ORF YOR326w [Saccharomyces cerevisiae]
23421	ENU07215	ANI61C7677: 49-68 4030..3702	49-68	457-479	LINAP	g607855	120	61	0.000000				(U11098) hydroxyindole-O-methyltransferase [Homo sapiens]
23422	ENU07216	ANI61S816:1..318			LINAP	g728913	135	74	4.00E-13	33	11		"MG(2+) transport ATPase, P-type 1 ; (AE000495) Mg2+ transport ATPase, P-type 1 [Escherichia coli] "
23423	ENU07217	ANI61C2621: 34-61 1731..3003	34-61	794-813	LINAP	g2132651	473	155	3.00E-37	33	47		probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae) ; (Z73133) ORF YLL028w [Saccharomyces cerevisiae]
23424	ENU07218	ANI61C3547: 52-71 3428..1912	52-71	766-785	LINAP	g140201	1005	206	8.00E-67	55	28		protein kinase YAK1 ; protein kinase YAK1 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) ; (X16056) Yak1 kinase (AA 1 - 807) [Saccharomyces cerevisiae] ; (X87371) protein kinase [Saccharomyces cerevisiae] ; (Z49417) ORF YJL141c [Saccharomyces cerevisiae]
23425	ENU07219	ANI61C7112: 114-133 1..425	114-133	360-380	LINAP	g4539606	195	73	8.00E-13	39	65		[Saccharomyces cerevisiae] (AL049522) hypothetical DNAJ domain protein [Schizosaccharomyces pombe]
23426	ENU07220	ANI61C2637: 106-126 1..497	106-126	452-476	LINAP	g2924449	42	37	0.1				(AL020222) PE_PGERS [Mycobacterium tuberculosis]

Genomic Annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23427	ENU07221	ANI61C7691: 22-47 2634..5362		647-666	LINAP		g3915963	1425	228	3.00E-59	47	16	ATP-dependent bile acid permease ; probable membrane protein YLL048c - yeast (Saccharomyces cerevisiae) ; (Z73153) ORF YLL048c [Saccharomyces cerevisiae]
23428	ENU07222	ANI61C8374: 29-48 36..1769		771-796	LINAP		g283065	1718	351	3.00E-96	64	40	3-isopropylmalate dehydratase (EC 4.2.1.33) - Phycomyces blakesleeanus ; (X53090) alpha-isopropylmalate isomerase (AA I-689) [Phycomyces blakesleeanus]
23429	ENU07223	ANI61S846:1. 68-89 .365		206-225	LINAP		g1363903	233	115	1.00E-25	51	24	"serine-type carboxypeptidase - Penicillium janthinellum ; carboxypeptidase S3, penicillopeptidase S3, CPD-S3 [Penicillium janthinellum, IBT 3991, Peptide, 481 aa] "

Table 6.1

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23430	ENU07224	ANI61C8374: 1922..2257	28-48	317-336	LINAP		g3135546	492	203	9.00E-52			(AF061918) Tn5 transposase [Plasposon pTnMod-OCm] ; (AF061919) Tn5 transposase [Plasposon pTnMod-OCm'] ; (AF061920) Tn5 transposase [Plasposon pTnMod-OGm] ; (AF061923) Tn5 transposase [Plasposon pTnMod-SmO] ; (AF061924) Tn5 transposase [Plasposon pTnMod-OTc] ; (AF061925) Tn5 transposase [Plasposon pTnMod-OTc'] ; (AF061926) Tn5 transposase [Plasposon pTnMod-OTp'] ; (AF061927) Tn5 transposase [Plasposon pTnMod-CmOTc] ; (AF061928) Tn5 transposase [Plasposon pTnMod-Cm'OTc] ; (AF061929) Tn5 transposase [Plasposon pTnMod-RCm] ; (AF061930) Tn5 transposase [Plasposon pTnMod-RKm'] ; (AF061931) Tn5 transposase [Plasposon pTnMod-RTp']
23431	ENU07225	ANI61S907:3 52..1			LINAP		g3914818	131	57	0.00000008			DNA-directed RNA polymerase I largest subunit ; (Y09103) largest subunit of RNA polymerase I (A) [Drosophila melanogaster]
23432	ENU07226	ANI61C7114: 482..1158			LINAP		g548771	577	117	1.00E-51	53	53	60S ribosomal protein L3-2 ; ribosomal protein L3 - fission yeast (Schizosaccharomyces pombe) ; (X57734) ribosomal protein L3 [Schizosaccharomyces pombe]
23433	ENU07227	ANI61C7698: 23-45 3196..1151	23-45	775-801	LINAP		g399299	1580	225	5.00E-74	61	26	chromosome region maintenance protein 1 ; (X15482) crml product [Schizosaccharomyces pombe]

GenBank - GenBank

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23434	ENU07228	ANI61C8392: 40-60 507..884	40-60	454-475	LINAP		g131768	35	66	2.00E-10			quininate permease (quininate transporter) ; quininate transport protein - Emericella nidulans ; (X13525) quininate permease [Emericella nidulans] probable malate oxidoreductase (NAD) (malic enzyme) (ME) ; malate dehydrogenase homolog YKL029c - yeast (Saccharomyces cerevisiae) ; (Z28029) ORF YKL029c [Saccharomyces cerevisiae] beta-glucan synthesis-associated protein KRE6 ; (D88490) CaKRE6 [Candida albicans] (AL023634) hypothetical protein [Schizosaccharomyces pombe] (Y16675) aflatoxin B1-aldehyde reductase [Homo sapiens] putative transporter YIL166C ; probable membrane protein YIL166c - yeast (Saccharomyces cerevisiae) ; (Z46921) unknown [Saccharomyces cerevisiae] (AF030886) telomere-associated recQ- like helicase [Ustilago maydis] (L13655) membrane protein [Saccharum hybrid cultivar H65-7052] (AJ223998) PCZA361.18 [Amycolatopsis orientalis] (AL023634) protein kinase dsk1 [Schizosaccharomyces pombe] (AJ001909) transcriptional activator [Aspergillus niger] (AJ223504) amino acid transporter [Amanita muscaria] (X89442) peptide synthetase [Metarhizium anisopliae]
23435	ENU07229	ANI61C2616: 22-45 2660..4618	22-45	802-829	LINAP		g547888	1218	130	4.00E-46	40	38	
23436	ENU07230	ANI61C7114: 22-49 3961..4544	22-49	536-563	LINAP		g2498505	179	51	2.00E-14	43	21	
23437	ENU07231	ANI61C7710: 36-55 2928..3343	36-55	456-479	LINAP		g3150252	77	55	0.000000	27	21	
23438	ENU07232	ANI61C2641: 30-49 1214..2159	30-49	806-828	LINAP		g3378617	463	107	2.00E-41	44	78	
23439	ENU07233	ANI61C7128: 47-66 669..1472	47-66	682-703	LINAP		g731893	414	108	7.00E-40	47	37	
23440	ENU07234	ANI61C7693: 26-53 3032..1965	26-53	796-815	LINAP		g2642224	173	90	2.00E-17	28	36	
23441	ENU07235	ANI61C8379: 22-47 1661..911	22-47	702-729	LINAP		g294845	220	74	1.00E-20	33	64	
23442	ENU07236	ANI61C2649: 24-43 1079..1544	24-43	453-479	LINAP		g2894166	70	75	4.00E-13			
23443	ENU07237	ANI61C7110: 22-49 1636..43	22-49	768-786	LINAP		g3150261	1132	241	4.00E-63	56	37	
23444	ENU07238	ANI61C8381: 25-44 355..666	25-44	432-451	LINAP		g2808634	72	56	0.000000	29	13	
23445	ENU07239	ANI61C2655: 33-52 1026..1	33-52	770-789	LINAP		g4468097	516	131	3.00E-40	42	45	
23446	ENU07240	ANI61C351:2 29-48 822..1	29-48	712-730	LINAP		g2342601	1597	194	9.00E-49	40	5	

Genomic Organization

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23447	ENU07241	ANI61C7141: 1134..2760	22-44	720-739	LINAP		g1351624	905	69	4.00E-11	45	23	hypothetical 122.9 KD protein C29E6.10C in chromosome I; (Z66525) unknown [Schizosaccharomyces pombe]
23448	ENU07242	ANI61C8385: 3918..3469	42-69	452-479	LINAP		g1723076	82	74	6.00E-13	32	27	hypothetical 57.3 KD protein GMC-type oxidoreductase CY50.03C; (Z77137) hypothetical protein Rv1279 [Mycobacterium tuberculosis]
23449	ENU07243	ANI61C7137: 1126..763	60-79	412-431	LINAP		g1197667	86	37	0.08			(U46857) vitellogenin [Anolis pulchellus]
23450	ENU07244	ANI61C8400: 1308..1782	45-64	430-449	LINAP		g1653955	94	43	0.001			(D90917) eukaryotic protein kinase [Synecocystis sp.]
23451	ENU07245	ANI61C3600: 768..1717	66-85	778-801	LINAP		g1552169	145	71	1.00E-11			(D42138) PIG-B [Homo sapiens]
23452	ENU07246	ANI61C7678: 2208..1435	25-44	710-729	LINAP		g2494084	259	147	7.00E-35	40	78	glycerate dehydrogenase (NADH-dependent hydroxypyruvate reductase) (HPR) (GDH) (hydroxypyruvate dehydrogenase) (glyoxylate reductase) (HPR-A)
23453	ENU07247	ANI61C2687: 376..1	32-56	383-403	LINAP		g1175425	159	84	5.00E-16	30	25	hypothetical 72.2 KD protein C12C2.05C in chromosome II; (Z54140) hypothetical protein [Schizosaccharomyces pombe]
23454	ENU07248	ANI61C3566: 5338..6011	32-54	488-507	LINAP		g130784	85	61	0.000000			Pyrimidine pathway regulatory protein 1; regulatory protein PPR1 - yeast (Saccharomyces cerevisiae); (X01739) regulatory protein (AA 1-904) [Saccharomyces cerevisiae]; (Z73186) ORF YLR014c [Saccharomyces cerevisiae]
23455	ENU07249	ANI61C7136: 827..1	36-55	698-725	LINAP		g2147662	535	209	2.00E-53	50	12	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium; (D83643) polyketide synthase [Colletotrichum lagenarium]

Gene = Oryza sativa

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23456	ENU07250	ANI61C7678: 5186..2864	22-47	797-824	LINAP		g136232	1429	285	3.00E-76	50	31	"potassium transport protein, low-affinity ; potassium transport protein TRK2, low-affinity - yeast (Saccharomyces cerevisiae) ; (M65215) TRK2 [Saccharomyces cerevisiae] ; (Z28275) ORF YKR050w [Saccharomyces cerevisiae] " (X62570) IFP53 [Homo sapiens]
23457	ENU07251	ANI61C3588: 22-47 1848..672	22-47	794-813	LINAP		g32709	1009	295	3.00E-79	59	54	
23458	ENU07252	ANI61C2675: 27-46 218..1168	27-46	802-829	LINAP		g3318897	290	95	1.00E-19	39	33	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain B, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain C, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain D, Phenol Hydroxylase From Trichosporon Cutaneum " (AJ002894) OsGRP2 [Oryza sativa]
23459	ENU07253	ANI61C8388: 22-43 1335..1755	22-43	439-457	LINAP		g2624328	125	43	2.00E-12			
23460	ENU07254	ANI61C8388: 5001..3984			LINAP		g2506137	281	123	1.00E-27	33	8	"Erythronolide synthase, modules 5 and 6 (ORF 3) (6-deoxyerythronolide B synthase III) (DEBS 3) ; 6-deoxyerythronolide B synthase III - Saccharopolyspora erythraea ; (X62569) 6-deoxyerythronolide B synthase III [Saccharopolyspora erythraea] " (AL031262) hypothetical protein [Schizosaccharomyces pombe]
23461	ENU07255	ANI61C7738: 941..1734			LINAP		g3417427	144	35	0.73	30	57	"Ankyrin, brain variant 2 (ankyrin B) (ankyrin, nonerythroid) " (hypothetical 269.9 KD protein in FKHI1-MET18 intergenic region ; probable membrane protein YIL129c - yeast (Saccharomyces cerevisiae) ; (Z38059) orf, len: 2376, CAl: 0.14 [Saccharomyces cerevisiae] " (L35053) endonuclease [Magnaporthe grisea]
23462	ENU07256	ANI61C7743: 41-60 1610..1993	41-60	431-450	LINAP		g231551	146	53	0.000001	29	9	
23463	ENU07257	ANI61C7740: 36-55 3137..1	36-55	711-730	LINAP		g731871	790	136	3.00E-31	32	11	
23464	ENU07258	ANI61C8420: 1..1751			LINAP		g522302	866	187	1.00E-46	42	23	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23465	ENU07259	ANI61C3612: 749..1	28-47	608-632	LINAP		g2440190	166	113	2.00E-24	35	13	(Z98602) putative protein transport protein sec7 homolog [Schizosaccharomyces pombe]
23466	ENU07260	ANI61C7168: 1075..1	22-43	713-732	LINAP		g549738	128	51	1.00E-13			hypothetical amino-acid permease in STE3-GIN10 intergenic region ; probable transport protein YKL174c - yeast (Saccharomyces cerevisiae) ; (Z26878) unknown [Saccharomyces cerevisiae] ; (Z28174) ORF YKL174c [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae]
23467	ENU07261	ANI61C7739: 777..1	71-90	646-673	LINAP		g2330791	457	171	9.00E-48	43	39	(Z98601) carboxypeptidase s precursor [Schizosaccharomyces pombe]
23468	ENU07262	ANI61C3597: 2921..2073	22-47	784-809	LINAP		g1652017	298	136	3.00E-31	33	87	(D90901) hypothetical protein [Synecocystis sp.]
23469	ENU07263	ANI61C7150: 321..2402	83-107	805-829	LINAP		g1213484	447	39	0.031			(U41740) trans-Golgi p230 [Homo sapiens] ; peripheral membrane protein p230 [Homo sapiens]
23470	ENU07264	ANI61C8351: 9042..8303	22-44	686-713	LINAP		g2132871	187	104	7.00E-22	36	47	probable membrane protein YOR059c - yeast (Saccharomyces cerevisiae) ; (Z74967) ORF YOR059c [Saccharomyces cerevisiae] ; (Z70678) YOR29-10 [Saccharomyces cerevisiae]
23471	ENU07265	ANI61C3638: 1001..600	22-48	452-479	LINAP		g3184056	90	78	3.00E-14			(AL023776) hypothetical protein [Schizosaccharomyces pombe]
23472	ENU07266	ANI61C7176: 1912..1502	24-48	424-448	LINAP		g3402751	120	79	2.00E-14	29	8	(AL031187) putative protein [Arabidopsis thaliana]
23473	ENU07267	ANI61C352:1 0337..11129	37-56	740-759	LINAP		g3023852	1460	268	3.00E-71	90	55	guanine nucleotide-binding protein beta subunit-like protein (cross-pathway control WD-repeat protein CPC-2) ; CPC2 protein - Neurospora crassa ; (X81875) CPC2 protein [Neurospora crassa]

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23474	ENU07268	ANI61C7151: 22-44 4911..4133	22-44	739-758	LINAP		g728850	166	43	0.002			"glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucosidase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) ; (Z38061) mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae] ; (U30626) glucoamylase [Saccharomyces cerevisiae var. diastaticus]"
23475	ENU07269	ANI61C8436: 22-47 1225..1548	22-47	459-479	LINAP		g731632	279	96	2.00E-19	53	20	hypothetical 57.0 KD protein in SOD2-RPL27 intergenic region ; hypothetical protein YHR009c - yeast (Saccharomyces cerevisiae) ; (U10400) Yhr009cp [Saccharomyces cerevisiae] (Z29098) transposase (putative) [Drosophila hydei] (Z98763) putative Inositol polyphosphate phosphatase [Schizosaccharomyces pombe] hypothetical 49.3 KD protein C30D11.06C in chromosome I ; hypothetical protein SPAC30D11.06c - fission yeast (Schizosaccharomyces pombe) ; (Z67961) hypothetical protein [Schizosaccharomyces pombe] hypothetical 70.2 KD protein C22E12.10C in chromosome I ; (Z70043) unknown
23476	ENU07270	ANI61C7182: 1867..908			LINAP		g436464	187	102	4.00E-21			[Schizosaccharomyces pombe]
23477	ENU07271	ANI61C7731: 57-76 1286..4662	57-76	805-823	LINAP		g2370558	1186	175	3.00E-52	46	22	[Schizosaccharomyces pombe] hypothetical 49.3 KD protein C30D11.06C in chromosome I ; hypothetical protein SPAC30D11.06c - fission yeast (Schizosaccharomyces pombe) ; (Z67961) hypothetical protein [Schizosaccharomyces pombe] hypothetical 70.2 KD protein C22E12.10C in chromosome I ; (Z70043) unknown
23478	ENU07272	ANI61C3629: 30-49 4217..3351	30-49	806-829	LINAP		g1351659	124	64	0.000000	32	50	[Schizosaccharomyces pombe] hypothetical 49.3 KD protein C30D11.06C in chromosome I ; hypothetical protein SPAC30D11.06c - fission yeast (Schizosaccharomyces pombe) ; (Z67961) hypothetical protein [Schizosaccharomyces pombe] hypothetical 70.2 KD protein C22E12.10C in chromosome I ; (Z70043) unknown
23479	ENU07273	ANI61C3668: 91-110 1190..445	91-110	703-725	LINAP		g1723522	566	212	2.00E-54	51	38	[Schizosaccharomyces pombe] hypothetical 70.2 KD protein C22E12.10C in chromosome I ; (Z70043) unknown
23480	ENU07274	ANI61C3642: 37-63 2958..5308	37-63	709-736	LINAP		g2117720	1875	305	3.00E-82	56	31	[Schizosaccharomyces pombe] glycogen phosphorylase (EC 2.4.1.1) - yeast (Saccharomyces cerevisiae) ; (U28371) Glycogen phosphorylase (Swiss Prot. accession number P06738) [Saccharomyces cerevisiae] (Y17317) polyketide synthase [Aspergillus fumigatus]
23481	ENU07275	ANI61C7178: 22-49 2739..278	22-49	803-829	LINAP		g3163925	609	108	7.00E-23	27	12	[Saccharomyces cerevisiae] (Y17317) polyketide synthase [Aspergillus fumigatus]

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23482	ENU07276	ANI61C8422: 360..1299	104-123	783-801	LINAP		g4097158	155	107	9.00E-23	26	12	(U46488) NrpS [Proteus mirabilis]
23483	ENU07277	ANI61C8422: 94-113	701-718		LINAP		g4499843	184	53	0.000003	27	37	(AJ011965) oxidoreductase [Claviceps purpurea]
23484	ENU07278	4025..4843			LINAP		g3618210	74	39	0.031	33	53	(AL031579) hypothetical protein [Schizosaccharomyces pombe]
23485	ENU07279	101..1990			LINAP		g482458	1195	167	2.00E-64	62	45	methionyl aminopeptidase (EC 3.4.11.18) 2 - rat ; (L10652) initiation factor 2 associated 67 kDa protein [Rattus rattus]
23486	ENU07280	ANI61C8417: 34-53	804-829		LINAP		g2408035	750	73	2.00E-12	30	29	(Z99163) probable beta-adaptin clathrin assembly protein [Schizosaccharomyces pombe]
23487	ENU07281	ANI61C3674: 23-45	460-483		LINAP		g1352731	63	52	0.000004	27	28	putative protein disulfide isomerase C1F5.02 precursor ; (Z68136) unknown [Schizosaccharomyces pombe]
23488	ENU07282	ANI61C7744: 22-46	460-479		LINAP		g4567282	92	49	0.000000			(AC006841) putative DNAB protein [Arabidopsis thaliana]
23489	ENU07283	5017..5324	807-829		LINAP		g2381494	1072	359	1.00E-98	60	47	(AB005589) Srw1 [Schizosaccharomyces pombe]
23490	ENU07284	2093..3226	448-467		LINAP		g417106	91	54	0.000000	27	71	2-haloalkanoic acid dehalogenase I (L-2-haloacid dehalogenase I) (halocarboxylic acid halohydrolyase I) (DEHCl) ; 2-haloacid dehalogenase (EC 3.8.1.2) I - Pseudomonas sp ; (M62908) 2-haloalkanoic acid dehalogenase I [Pseudomonas sp.] sericin MG-2 - greater wax moth (fragments)
23491	ENU07285	ANI61C3654: 31-50	703-726		LINAP		g1083944	136	38	0.06			(AE001142) glutamyl-tRNA synthetase (gltX) [Borrelia burgdorferi]
23492	ENU07286	2860..3613	784-811		LINAP		g2688265	622	191	5.00E-50	44	47	(AL034443) putative integral membrane efflux protein [Streptomyces coelicolor]
23493	ENU07287	1411..267	710-730		LINAP		g4007671	186	50	2.00E-12	26	43	
		ANI61C3645: 25-44											
		3080..3830											

Genomic Annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23494	ENU07288	ANI61C7797: 1..319			LINAP		g731649	102	61	0.000000	28	22	hypothetical 53.4 KD protein in SLT2-PUT2 intergenic region ; hypothetical protein YHR036w - yeast (Saccharomyces cerevisiae) ; (U00062) Yhr036wp [Saccharomyces cerevisiae] protein kinase DSK1 (DIS1-suppressing protein kinase) ; dis1-suppressing protein kinase dsk1 - fission yeast (Schizosaccharomyces pombe) ; (D13447) protein kinase [Schizosaccharomyces pombe] (Z95436) hypothetical protein Rv3633 [Mycobacterium tuberculosis] hypothetical 78.3 KD protein in RIP1-URA3 intergenic region ; hypothetical protein YEL023c - yeast (Saccharomyces cerevisiae) ; (U18530) Yel023cp [Saccharomyces cerevisiae] Topoisomerase I-related protein TRF4 ; topoisomerase I-related protein TRF4 - yeast (Saccharomyces cerevisiae) ; (Z48149) ORF [Saccharomyces cerevisiae] ; (U31355) Trf4p [Saccharomyces cerevisiae] ; (Z74857) ORF YOL115w [Saccharomyces cerevisiae] (AC000133) ORF [Emericella nidulans] sodium/potassium-transporting ATPase alpha chain (sodium PUMP) (NA+/K+ ATPase) ; Na+/K+-exchanging ATPase (EC 3.6.1.37) alpha chain - white sucker ; (X58629) adenosinetriphosphatase [Catostomus commersoni] (L35601) ankyrin [Drosophila melanogaster] ; ankyrin [Drosophila melanogaster]
23495	ENU07289	ANI61C8443: 1..410	137-164	364-389	LINAP		g544191	109	68	2.00E-11	37	21	
23496	ENU07290	ANI61C3624: 22-48 7327..7005	455-477		LINAP		g2105061	69	54	0.000000	29	40	
23497	ENU07291	ANI61C3690: 22-49 1906..1	713-730		LINAP		g731409	261	63	0.000000	22	36	
23498	ENU07292	ANI61C7806: 23-45 2837..1468	611-630		LINAP		g1717744	299	152	3.00E-36	35	43	
23499	ENU07293	ANI61C3682: 22-46 1684..2391	660-687		LINAP		g1870209	265	48	0.000000			
23500	ENU07294	ANI61C7809: 25-52 3008..3729	676-701		LINAP		g114386	221	57	4.00E-18	36	21	
23501	ENU07295	ANI61C3648: 22-41 6002..4666	762-789		LINAP		g557084	387	90	2.00E-17			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23502	ENU07296	ANI61C7778: 32-51 7591..4646	32-51	768-788	LINAP		g2133248	2998	267	8.00E-71	66	26	chitin synthase (EC 2.4.1.16) C - Aspergillus fumigatus ; (X94245) chitin synthase C [Aspergillus fumigatus]
23503	ENU07297	ANI61C3644: 37-56 5841..6454	37-56	568-593	LINAP		g2645229	502	146	2.00E-34	37	41	(U78597) kinesin light chain [Plectonema boryanum]
23504	ENU07298	ANI61C7841: 22-45 1..460	22-45	372-391	LINAP		g1145799	61	48	0.00005	31	20	(U41806) p60 [Homo sapiens]
23505	ENU07299	ANI61C8492: 104-123 828..1277	104-123	315-338	LINAP		g1870209	625	231	2.00E-60	92	27	(AC000133) ORF [Emericella nidulans]
23506	ENU07300	ANI61C3677: 22-44 2990..1456	22-44	802-829	LINAP		g4107287	167	124	7.00E-28	30	54	(AL035076) putative allantoate permease [Schizosaccharomyces pombe]
23507	ENU07301	ANI61C8488: 22-44 2067..1752	22-44	419-438	LINAP		g2702312	60	49	0.00002			(U76556) antigen N54 [Neospora sp.]
23508	ENU07302	ANI61C3705: 102-120 1..655	102-120	590-609	LINAP		g464786	179	95	4.00E-19	33	33	SPT10 protein ; regulatory protein SPT10 - yeast (Saccharomyces cerevisiae) ; (L24435) SPT10 [Saccharomyces cerevisiae] ; (Z49402) ORF YJL127c [Saccharomyces cerevisiae]
23509	ENU07303	ANI61C7845: 24-44 1409..1091	24-44	267-294	LINAP		g3581903	189	84	3.00E-16	42	17	(AL031545) DEAD box ATP-dependent RNA helicase [Schizosaccharomyces pombe]
23510	ENU07304	ANI61C3693: 22-44 5491..6885	22-44	635-654	LINAP		g117619	305	77	2.00E-18	29	45	choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
23511	ENU07305	ANI61C7850: 28-51 814..1452	28-51	589-608	LINAP		g1805251	348	162	2.00E-39	40	38	(U58946) transposase [Aspergillus awamori]
23512	ENU07306	ANI61C7862: 671..286			LINAP		g1084952	88	76	1.00E-13			hypothetical protein YPR031w - yeast (Saccharomyces cerevisiae) ; (Z49274) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]

Sequence Annotation

Seq num	Seq id	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23513	ENU07307	Contig source ANI61C7819: 48-72 1485..2608	807-829	LINAP		g1346290	364	72	3.00E-23	28	42	high-affinity glucoSE transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis] (AF052688) putative transmembrane transporter Liz1p
23514	ENU07308	ANI61C3737: 63-82 1184..287	765-784	LINAP		g2981103	202	65	6.00E-10	27	43	[Schizosaccharomyces pombe] ; (AL023706) transmembrane transporter Liz1p [Schizosaccharomyces pombe] (AL021409) polyketide synthase [Streptomyces coelicolor]
23515	ENU07309	ANI61C8485: 25-52 5622..3617	804-829	LINAP		g2808753	601	112	4.00E-24	31	11	probable membrane protein YDL133w - yeast (Saccharomyces cerevisiae) ; (X96876) putative ORF [Saccharomyces cerevisiae] ; (Z74181) ORF YDL133w [Saccharomyces cerevisiae]
23516	ENU07310	ANI61C3786: 22-44 932..1412	366-385	LINAP		g2132440	183	96	2.00E-19	33	37	aminopeptidase Y precursor ; aminopeptidase Y (EC 3.4.11.-) - yeast (Saccharomyces cerevisiae) ; (L31635) aminopeptidase Y [Saccharomyces cerevisiae] ; (X76053) YBR2024-ORF [Saccharomyces cerevisiae] ; (Z36155) ORF YBR286w [Saccharomyces cerevisiae] ; ORF YBR2024 [Saccharomyces cerevisiae] (Z69254) alpha-galactosidase [Hypocrea jecorina] (AF023132) choline monoxygenase [Beta vulgaris]
23517	ENU07311	ANI61C7870: 31-51 1128..2120	808-825	LINAP		g584764	542	212	3.00E-54			"lignostilbene alphabeta-dioxygenase (EC 1.13.11.43) III isozyme beta chain - Pseudomonas paucimobilis ; (S80637) lignostilbene-alpha,beta-dioxygenase isozyme III, LSD-III [Pseudomonas paucimobilis, TMY1009, Peptide, 489 aa] [Sphingomonas paucimobilis] "
23518	ENU07312	ANI61C3744: 90-109 843..1	712-731	LINAP		g1580818	674	245	3.00E-69	55	33	
23519	ENU07313	ANI61C8510: 24-51 3106..2623	449-476	LINAP		g2522210	111	48	0.000000			
23520	ENU07314	ANI61C3730: 24-50 1373..619	686-713	LINAP		g2120665	447	189	1.00E-47	44	46	

Gene annotation

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23521	ENU07315	ANI61C787:1 418..3186	22-49	803-829	LINAP		g3581916	1423	250	7.00E-66	44	22	(AL031545) muts family DNA mismatch repair protein
23522	ENU07316	ANI61C7869: 22-46 2737..1530		799-817	LINAP		g3318897	95	80	2.00E-14	31	36	[Schizosaccharomyces pombe] "Chain A, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain B, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain C, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain D, Phenol Hydroxylase From Trichosporon Cutaneum "
23523	ENU07317	ANI61C3743: 39-59 1466..3481		774-793	LINAP		g1352290	916	157	9.00E-38	38	27	DNA ligase I (polydeoxyribonucleotide synthase (ATP)) ; DNA ligase (ATP) (EC 6.5.1.1) I - mouse ; (U19604) DNA ligase I [Mus musculus] ; (U04674) DNA ligase I [Mus musculus]
23524	ENU07318	ANI61C7892: 22-47 1050..591		443-462	LINAP		g1352493	224	95	4.00E-19	36	16	"type II inositol-1,4,5-trisphosphate 5-phosphatase precursor (5PTase) ; (M74161) inositol polyphosphate 5-phosphatase [Homo sapiens] " myo-inositol transporter 2 ; (Z95334) Itr2p [Schizosaccharomyces pombe] (U24167) PAK1 [Saccharomyces cerevisiae] (U41748) coded for by C. elegans cDNA yk16f8.5; coded for by C. elegans cDNA yk55f7.5; coded for by C. elegans cDNA yk16f8.3; coded for by C. elegans cDNA yk55f7.3; coded for by C. elegans cDNA yk72a5.5; coded for by C. elegans cDNA yk72a5.3...
23525	ENU07319	ANI61C7898: 451..1			LINAP		g3219812	69	56	0.000000	26	21	
23526	ENU07320	ANI61C7913: 22-42 1522..1		620-637	LINAP		g862488	847	42	0.000000	46	12	
23527	ENU07321	ANI61C8507: 22-47 1205..896		438-457	LINAP		g1118141	51	32	3.1			
23528	ENU07322	ANI61C7899: 23-50 1..1557		794-813	LINAP		g3004863	722	238	4.00E-62	45	33	"(AF029354) exo-beta-1,3-glucanase [Ampelomyces quisqualis] "
23529	ENU07323	ANI61C7929: 22-44 1461..2302		620-643	LINAP		g3914984	282	92	2.00E-28	30	7	Ferrichrome siderophore peptide synthetase ; (U62738) ferrichrome siderophore peptide synthetase [Ustilago maydis]

Gene Description

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23530	ENU07324	ANI61C8542: 1743..828	68-87	801-820	LINAP		g1350789	322	148	5.00E-35	36	62	"mitochondrial 60S ribosomal protein L3 precursor (YML3) ; ribosomal protein YmL3, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z49211) Mrlp3p [Saccharomyces cerevisiae] " (AF008228) odd Oz protein [Drosophila melanogaster]
23531	ENU07325	ANI61C8533: 58-77 3468..3161	58-77	459-478	LINAP		g2266927	64	46	0.0001	27	3	"leucyl-TRNA synthetase, cytoplasmic (leucine--TRNA ligase) (LEURS) ; leucine--tRNA ligase (EC 6.1.1.4), cytosolic - Neurospora crassa ; (M30473) leucyl-tRNA synthetase [Neurospora crassa] " (AF017777) small optic lobes [Drosophila melanogaster]
23532	ENU07326	ANI61C7922: 24-51 4782..5315	24-51	438-465	LINAP		g135140	540	203	9.00E-52	60	15	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata] " (cytochrome P450 XVIIA1 (P450-C17) (steroid 17-alpha-hydroxylase/17,20 lyase) ; steroid 17alpha-monooxygenase (EC 1.14.99.9) cytochrome P450 17 - rainbow trout ; (X65800) steroid 17-alpha-monooxygenase [Oncorhynchus mykiss] " probable membrane protein YOL060c - yeast (Saccharomyces cerevisiae) ; (X91067) 01216; hypothetical protein [Saccharomyces cerevisiae] ; (Z74802) ORF YOL060c [Saccharomyces cerevisiae]
23533	ENU07327	ANI61C8533: 81-103 4656..4194	81-103	419-442	LINAP		g3004662	110	50	6.00E-11	36	7	"glucan 1,3-beta-glucosidase precursor (exo-beta 1,3 glucanase) (1,3-beta-D-glucanohydrolase) ; (L48994) exo-beta 1,3 glucanase [Cochliobolus carbonum] " (Z98980) hypothetical protein [Schizosaccharomyces pombe]
23534	ENU07328	ANI61C8536: 66-85 3309..1177	66-85	782-804	LINAP		g1166378	840	205	3.00E-52	41	25	
23535	ENU07329	ANI61C858: 8 24-45 72..320	24-45	490-509	LINAP		g231902	95	41	0.000007			
23536	ENU07330	ANI61C8544: 43-70 3861..2610	43-70	807-829	LINAP		g2132836	1101	322	1.00E-92	65	37	
23537	ENU07331	ANI61C8586: 91-1114 2116..1322	91-1114	750-773	LINAP		g1352399	168	101	5.00E-21	32	26	
23538	ENU07332	ANI61C8567: 29-51 4390..6002	29-51	734-758	LINAP		g2388984	317	66	3.00E-10	31	25	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23539	ENU07333	ANI61C8567: 1381..3558	22-44	810-829	LINAP		g2388584	133	35	0.61			(AC000098) EST gb ATTS1136 comes from this gene. [Arabidopsis thaliana]
23540	ENU07334	ANI61C8572: 30-49	30-49	767-791	LINAP		g2507070	236	91	8.00E-18	29	50	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
23541	ENU07335	ANI61C8570: 28-55	28-55	436-457	LINAP		g1351653	160	100	6.00E-21			hypothetical 103.2 KD protein C24B11.10C in chromosome I ; hypothetical protein SPAC24B11.10c - fission yeast (Schizosaccharomyces pombe) ; (Z67757) unknown [Schizosaccharomyces pombe]
23542	ENU07336	ANI61C8596: 3531..2592	22-43	806-827	LINAP		g1351714	85	87	1.00E-16			putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
23543	ENU07337	ANI61C8593: 2431..3221	22-48	748-769	LINAP		g731532	813	164	2.00E-72	54	30	putative 90.2 KD zinc finger protein in CCA1-ADK2 intergenic region ; hypothetical protein YER169w - yeast (Saccharomyces cerevisiae) ; (U18922) Yer169wp [Saccharomyces cerevisiae] probable protein-tyrosine phosphatase YBR276C ; probable protein-tyrosine-phosphatase (EC 3.1.3.48) - yeast (Saccharomyces cerevisiae) ; (X76053) YBR2013-ORF [Saccharomyces cerevisiae] ; (Z36145) ORF YBR276c [Saccharomyces cerevisiae] ; ORF YBR2013 [Saccharomyces cerevisiae]
23544	ENU07338	ANI61C8552: 516..1	31-51	391-413	LINAP		g586390	99	89	2.00E-17	36	16	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23545	ENU07339	ANI61C8585: 6129..7445	23-47	775-794	LINAP		g114301	877	269	2.00E-71	61	25	calcium-transporting ATPase 1 (GOLGI CA2+-ATPase) ; Ca2+-transporting ATPase (EC 3.6.1.38) PMR1 - yeast (Saccharomyces cerevisiae) ; (M25488) PMR1 protein [Saccharomyces cerevisiae] ; (X85757) calcium transporting ATPase 1 [Saccharomyces cerevisiae] ; (Z72690) ORF YGL167c [Saccharomyces cerevisiae]
23546	ENU07340	ANI61C86:53 0.4337	23-46	768-787	LINAP		g4107308	1329	106	3.00E-22	29	18	(AL035075) hypothetical TPR domain-containing protein [Schizosaccharomyces pombe]
23547	ENU07341	ANI61C8621: 3687..3212	56-75	406-425	LINAP		g1708909	184	100	7.00E-21	30	35	malic acid transport protein (malate permease) ; C4-dicarboxylate transport protein mae1 - fission yeast (Schizosaccharomyces pombe) ; (U21002) malic acid transport protein [Schizosaccharomyces pombe]
23548	ENU07342	ANI61C8630: 41-61 584..1	41-61	456-475	LINAP		g1934614	139	106	1.00E-22	33	17	(U93874) cytochrome P450 102 [Bacillus subtilis] ; (Z99117) similar to cytochrome P450 / NADPH-cytochrome P450 reductase [Bacillus subtilis]
23549	ENU07343	ANI61C864:1 ..337	39-59	296-315	LINAP		g119830	105	62	0.000000			"fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41] ; fatty-acid synthase (EC 2.3.1.85) - Penicillium griseofulvum ; (M37461) FAS2 protein [Penicillium patulum] " (AJ223999) PCZA363.3 [Amycolatopsis orientalis]
23550	ENU07344	ANI61C8641: 396..894	52-71	456-477	LINAP		g2894188	81	42	0.000002			hypothetical 54.3 KD TRP-ASP repeats containing protein C17H9.19C in chromosome I ; (L75944) WD repeat protein [Schizosaccharomyces pombe] ; (Z98597) beta-transducin [Schizosaccharomyces pombe]
23551	ENU07345	ANI61C8625: 1107..2494	72-92	789-808	LINAP		g3219975	283	87	1.00E-16	33	41	

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23552	ENU07346	ANI61C1037 4:3791..4541	48-67	703-730	LINAP		g3876092	350	108	1.00E-35	43	30	(Z69635) Similarity to Drosophila white protein (SW:WHIT_DROME); cDNA EST EMBL:M89346 comes from this gene; cDNA EST yk311f2.3 comes from this gene; cDNA EST yk311f2.5 comes from this gene [Caenorhabditis elegans] hypothetical protein YLR074c - yeast (Saccharomyces cerevisiae) ; (Z73246) ORF YLR074c [Saccharomyces cerevisiae]
23553	ENU07347	ANI61C1038 3:4832..4388	22-49	458-476	LINAP		g2131767	116	55	0.000000	37	62	Serine/threonine protein phosphatase PP-X isozyme 1 ; phosphoprotein phosphatase (EC 3.1.3.16) X-1 (clone EP129) - Arabidopsis thaliana ; (Z22587) protein phosphatase [Arabidopsis thaliana] ; (AF030289) protein phosphatase X isoform 1 [Arabidopsis thaliana] ; (AL035440) phosphoprotein phosphatase (PPX-1) [Arabidopsis thaliana] hypothetical protein YLR423c - yeast (Saccharomyces cerevisiae) ; (U20939) Ylr423cp [Saccharomyces cerevisiae] chromosome segregation protein CUT3 ; cut3 protein - fission yeast (Schizosaccharomyces pombe) ; (D30788) cut3 protein [Schizosaccharomyces pombe] General amino-acid permease GAP1 ; amino acid transport protein GAP1 - yeast (Saccharomyces cerevisiae) ; (Z28264) ORF YKR039w [Saccharomyces cerevisiae]
23554	ENU07348	ANI61C1040 7:1418..1956			LINAP		g1346782	1092	201	2.00E-51			"[L76169] reverse transcriptase, RNaseH (Glomerella cingulata) " hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae) ; (U10400) Ysc84p [Saccharomyces cerevisiae]
23555	ENU07349	ANI61C1040 2:2381..2038	22-46	449-468	LINAP		g1078089	98	52	0.000004	26	33	
23556	ENU07350	ANI61C43:32 06..147	31-51	771-793	LINAP		g729230	1899	86	4.00E-25	24	20	
23557	ENU07351	ANI61C1041 4:1..857			LINAP		g544369	474	200	9.00E-51	40	46	
23558	ENU07352	ANI61C1040 4:5613..5130	59-86	436-463	LINAP		g1166378	135	94	4.00E-19	31	14	
23559	ENU07353	ANI61C1041 3:1682..783	22-42	802-829	LINAP		g626598	394	111	3.00E-36	42	53	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23560	ENU07354	ANI61C1041 3:2409..2019	51-70	457-479	LINAP		g4538664	180	71	7.00E-12	32	91	(AL049474) hypothetical protein [Schizosaccharomyces pombe]
23561	ENU07355	ANI61C4342: 1104..1732	22-48	588-608	LINAP		g2645229	241	87	5.00E-23	37	41	(U78597) kinesin light chain [Plectonema boryanum]
23562	ENU07356	ANI61C1041 0:3562..3158	45-64	363-382	LINAP		g1055333	111	68	6.00E-11	25	23	(U38821) pig1 [Magnaporthe grisea]
23563	ENU07357	ANI61C4349: 1384..628	22-47	714-733	LINAP		g2506204	265	94	2.00E-24	38	68	hypothetical 33.4 KD protein in MOEA-GRXA intergenic region precursor ; (AE000185) putative asparaginase [Escherichia coli] ; (D90720) Hypothetical protein in moeA-grxA intergenic region precursor . [Escherichia coli] ; (D90721) Hypothetical protein in moeA-grxA intergenic region precursor . [Escherichia coli]
23564	ENU07358	ANI61C1042 5:2784..2396	45-64	425-446	LINAP		g3025094	314	138	1.00E-32	51	50	hypothetical 32.5 KD protein in MSH6-BMH2 intergenic region ; thioredoxin homolog YDR098c - yeast (Saccharomyces cerevisiae) ; (Z47746) probable thioredoxin [Saccharomyces cerevisiae]
23565	ENU07359	ANI61C1040 9:4217..4878	24-43	616-635	LINAP		g1711596	212	134	7.00E-31	36	28	putative sulfate transporter YPR003C ; probable membrane protein YPR003c - yeast (Saccharomyces cerevisiae) ; (Z48951) unknown [Saccharomyces cerevisiae] ; (U31900) Lpz3p [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae] (AF024618) cyclin H [Drosophila melanogaster]
23566	ENU07360	ANI61C1043: 2600..3276	22-47	602-621	LINAP		g2570798	222	53	0.000000	30	51	putative dioxygenase YLL057C ; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae) ; (Z47973) ORF L0572 [Saccharomyces cerevisiae] ; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]
23567	ENU07361	ANI61C1038 8:9158..8406	47-65	684-703	LINAP		77				25		
23568	ENU07362	ANI61C433:5 523..6762	47-66	805-829	LINAP		g2497056	613	131	2.00E-46	44	57	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23569	ENU07363	ANI61C4387: 415..1	22-49	455-474	LINAP		g3169083	124	84	7.00E-16	37	42	(AL023705) hypothetical protein [Schizosaccharomyces pombe]
23570	ENU07364	ANI61C4384: 1566..2087	67-86	468-487	LINAP		g3023956	166	76	2.00E-13	36	11	vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospora anserina]
23571	ENU07365	ANI61C1043: 4:4998..4685	70-89	320-339	LINAP		g4154042	123	65	3.00E-10	34	33	(AL035159) putative oxidoreductase [Mycobacterium leprae]
23572	ENU07366	ANI61C436:3 921..3166	38-57	689-708	LINAP		g2634106	189	121	6.00E-27	29	9	(Z99113) polyketide synthase [Bacillus subtilis]
23573	ENU07367	ANI61C436:6 570..5307	29-48	804-823	LINAP		g1546072	275	211	6.00E-54	43	10	(U68040) polyketide synthase [Cochliobolus heterostrophus]
23574	ENU07368	ANI61C4410: 1381..3045	22-47	782-801	LINAP		g2342601	1238	213	9.00E-55	36	5	(X89442) peptide synthetase [Metarhizium anisopliae]
23575	ENU07369	ANI61C4402: 2740..3699	95-114	726-745	LINAP		g3702646	193	68	3.00E-19			(AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
23576	ENU07370	ANI61C4429: 1..704	110-137	645-664	LINAP		g417253	136	73	3.00E-12	41	24	lipase 5 precursor ; triacylglycerol lipase (EC 3.1.1.3) 5 precursor - yeast (Candida rugosa)
23577	ENU07371	ANI61C1046: 4:1629..1300	48-73	449-468	LINAP		g3550483	80	54	0.000000			(AJ224324) cp31BHv [Hordeum vulgare]
23578	ENU07372	ANI61C4444: 602..208	22-44	454-479	LINAP		g2558841	172	99	2.00E-20	41	8	(AF016585) polyketide synthase module 6 [Streptomyces caelestis]
23579	ENU07373	ANI61C1044: 1:3768..4364	51-70	508-527	LINAP		g3912992	122	92	3.00E-18			alpha-glucosidase (maltase) ; (AF042494) alpha-glucosidase [Sulfolobus solfataricus]
23580	ENU07374	ANI61C4446: 1415..392	25-45	719-743	LINAP		g2440190	372	78	1.00E-29	36	15	(Z98602) putative protein transport protein sec7 homolog [Schizosaccharomyces pombe]
23581	ENU07375	ANI61C1045: 1:2702..2370	23-46	442-461	LINAP		g1169369	40	50	0.00001	35	23	DNAJ protein ; heat shock protein dnaJ - Clostridium acetobutylicum ; (X69050) DnaJ [Clostridium acetobutylicum]
23582	ENU07376	ANI61C1100: 0:2307..3900	22-45	804-827	LINAP		g3426176	354	52	0.000004			(AB008771) beta-N-Acetylglucosaminidase [Streptomyces thermoviolaceus]
23583	ENU07377	ANI61C1104: 2:1321..657	109-128	622-644	LINAP		g3130007	147	43	0.002			(AL023517) putative secreted protease [Streptomyces coelicolor]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23584	ENU07378	ANI61C4476:258..558	36-57	277-300	LINAP		g4097335	89	47	0.00009	36	50	(U57524) I kappa B alpha [Mus musculus]
23585	ENU07379	ANI61C1104:0:1..460	47-70	401-419	LINAP		g1708078	81	50	0.00001	28	7	"endoglucanase A precursor (endo-1,4-beta-glucanase A) (cellulase A) ; (L32742) cellulase [Caldocellum saccharolyticum] "
23586	ENU07380	ANI61C4496:1..886	112-131	804-829	LINAP		g4503355	109	104	8.00E-22	26	15	dedicator of cyto-kinesis 1 ; (D50857) DOCK180 protein [Homo sapiens]
23587	ENU07381	ANI61C1046:2:4242..4589	36-59	457-479	LINAP		g4249377	124	42	0.000000	37	25	(AC005966) Similar to gi 2829865 F3I6.4 from Arabidopsis thaliana BAC gb AC002396. [Arabidopsis thaliana]
23588	ENU07382	ANI61C439:1..473	130-157	432-452	LINAP		g3413518	417	118	3.00E-26	37	9	(AB010810) phospholipase D [Candida albicans]
23589	ENU07383	ANI61C1102:9:4141..4735	22-49	501-525	LINAP		g1711639	663	275	2.00E-73	72	23	"methionyl-TRNA synthetase, cytoplasmic (methionine--TRNA ligase) (METRS) ; methionine--TRNA ligase (EC 6.1.1.10), cytosolic - yeast (Saccharomyces cerevisiae) ; (Z73049) ORF YGR264c [Saccharomyces cerevisiae] ; (Y07777) methionine--tRNA ligase [Saccharomyces cerevisiae] "
23590	ENU07384	ANI61C45:1..535	102-122	404-423	LINAP		g1710803	150	52	1.00E-12	36	29	retrograde regulation protein 2 ; RTG2 protein - yeast (Saccharomyces cerevisiae) ; (X94357) ORF NRF588; EMBL:SCRTG2X:M97691; PIR:B44344;B44344 [Saccharomyces cerevisiae] ; (M97691) Rtg2p [Saccharomyces cerevisiae] ; (Z72774) ORF YGL252c [Saccharomyces cerevisiae]
23591	ENU07385	ANI61C1046:8:1..831	102-125	782-803	LINAP		g2497953	347	143	3.00E-37	45	37	molybdopterin biosynthesis CNX1 protein (molybdenum cofactor biosynthesis enzyme CNX1) ; (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] ; (AJ236870) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana]

Gene description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23592	ENU07386	ANI61C45:15 62..1195	22-49	454-479	LINAP		g1911486	159	45	0.000000	38	38	"(S80872) putative Tc1-mariner class transposase/IS630-Tc1 homolog [Aspergillus niger, chlorate-resistant mutant 46, transposon Ant1, Peptide Transposon, 325 aa] [Aspergillus niger]"
23593	ENU07387	ANI61C4537: 1259..2507	40-59	805-825	LINAP		g2132480	553	124	9.00E-28	43	33	probable membrane protein YDR205w - yeast (Saccharomyces cerevisiae) ; (Z68194) unknown [Saccharomyces cerevisiae]
23594	ENU07388	ANI61C1046 5:2048..718	22-42	800-827	LINAP		g2131433	692	244	7.00E-64	44	40	hypothetical protein YDR332w - yeast (Saccharomyces cerevisiae) ; (U32517) Ydr332wp [Saccharomyces cerevisiae]
23595	ENU07389	ANI61C4532: 2747..726	22-48	810-829	LINAP		g3913674	217	46	0.0002			Ferric reductase transmembrane component 3 precursor ; probable membrane protein YOR381w - yeast (Saccharomyces cerevisiae) ; (Z75289) ORF YOR381w [Saccharomyces cerevisiae]
23596	ENU07390	ANI61C1046 5:7103..6296	26-45	764-783	LINAP		g4220848	609	169	7.00E-48	49	16	(AF033823) moira [Drosophila melanogaster]
23597	ENU07391	ANI61C4588: 413..1	55-79	452-479	LINAP		g2131783	706	88	3.00E-26	46	31	hypothetical protein YLR116w - yeast (Saccharomyces cerevisiae) ; (U53877) Ylr116wp [Saccharomyces cerevisiae] ; (X89514) putative orf [Saccharomyces cerevisiae] ; (Z73288) ORF YLR116w [Saccharomyces cerevisiae]
23598	ENU07392	ANI61C1047 8:2773..3779	24-42	801-828	LINAP		g121967	81	33	2.3			histone H2A.1 ; histone H2A.1 - yeast (Saccharomyces cerevisiae) ; (V01304) histone H2A1 [Saccharomyces cerevisiae] ; (U13239) histone H2A1 [Saccharomyces cerevisiae] ; (Z48612) H2a1p [Saccharomyces cerevisiae]
23599	ENU07393	ANI61C5459: 1128..550	178-202	535-558	LINAP		g2440180	187	37	0.13			(Z99531) ubiquitin system protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23600	ENU07394	ANI61C1103 2:6045..6458	68-95	455-479	LINAP		g1710802	121	75	3.00E-13	35	45	RTA1 protein ; RTA1 protein - yeast (Saccharomyces cerevisiae) ; (Z72998) ORF YGR213c [Saccharomyces cerevisiae] ; (X84736) RTA1 [Saccharomyces cerevisiae] (AB025252) reverse transcriptase [Magnaporthe grisea] (U43704) ketoreductase [Streptomyces sp. C5] (AC004392) Contains similarity to gb U51898 Ca2+-independent phospholipase A2 from Rattus norvegicus. [Arabidopsis thaliana] (AF111172) lysosomal pepstatin insensitive protease precursor [Mus musculus]
23601	ENU07395	ANI61C532:4 143..3695	22-46	457-479	LINAP		g4586458	133	89	2.00E-17	32	57	Transmission-blocking target antigen S230 precursor ; transmission-blocking target antigen Pfs230 - Plasmodium falciparum ; (L08135) Pfs230 [Plasmodium falciparum] ; (L04162) s230 [Plasmodium falciparum] ; (AE001393) transmission blocking target antigen Pfs230 [Plasmodium falciparum]
23602	ENU07396	ANI61C1103 5:2574..3119	22-49	499-525	LINAP		g1163927	108	75	3.00E-13			(AL021046) putative mitotic spindle protein [Schizosaccharomyces pombe]
23603	ENU07397	ANI61C532:1 1195..11988	22-49	750-773	LINAP		g3367519	96	72	4.00E-12	30	20	"Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 1 ; (L43920) microsomal omega-6 desaturase [Glycine max] "
23604	ENU07398	ANI61C4578: 2040..1151	62-88	810-829	LINAP		g4106913	285	46	0.00005	33	17	lymphocyte specific helicase - mouse ; (U25691) lymphocyte specific helicase [Mus musculus]
23605	ENU07399	ANI61C5492: 1..785	51-70	716-735	LINAP		g730413	118	52	0.000004			
23606	ENU07400	ANI61C5469: 1442..576	22-48	803-829	LINAP		g2706463	297	125	4.00E-28	27	19	
23607	ENU07401	ANI61C1107 5:2077..2843	23-49	689-706	LINAP		g1345976	371	187	8.00E-47	44	59	
23608	ENU07402	ANI61C4539: 3779..5452	22-49	809-829	LINAP		g2137490	700	266	1.00E-70	50	44	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23609	ENU07403	ANI61C5517: 24-47 876..1	24-47	776-798	LINAP		g1346360	638	201	3.00E-54	53	43	probable serine/threonine-protein kinase C24B11.11c ; hypothetical protein SPAC24B11.11c - fission yeast (Schizosaccharomyces pombe) ; (Z67757) unknown
23610	ENU07404	ANI61C1048 2:2761..4048	22-49	810-829	LINAP		g1168808	446	155	5.00E-37	39	40	[Schizosaccharomyces pombe] cell division control protein 18 ; cell division control protein CDC18+ - fission yeast (Schizosaccharomyces pombe) ; (L16793) cell division cycle protein [Schizosaccharomyces pombe] ; (AL022305) cell division control protein 18 [Schizosaccharomyces pombe]
23611	ENU07405	ANI61C4614: 57-83 1..458	57-83	411-437	LINAP		g4063383	174	61	7.00E-10	53	30	(AF096285) serine-threonine kinase receptor-associated protein [Mus musculus]
23612	ENU07406	ANI61C5521: 22-45 455..1028	22-45	360-379	LINAP		g586352	474	137	1.00E-44	56	15	hypothetical 124.0 KD protein in PCS60-ABD1 intergenic region ; probable membrane protein YBR235w - yeast (Saccharomyces cerevisiae) ; (Z36104) ORF YBR235w [Saccharomyces cerevisiae]
23613	ENU07407	ANI61C4601: 55-72 330..1	55-72	444-463	LINAP		g3023267	109	61	0.000000	37	10	alpha-glucosidase precursor (maltase) ; (D45356) alpha-glucosidase [Aspergillus niger]
23614	ENU07408	ANI61C5535: 22-40 388..982	22-40	550-574	LINAP		g4104775	96	57	0.000000	31	37	(AF039534) salicylate hydroxylase [Pseudomonas stutzeri]
23615	ENU07409	ANI61C4618: 45-64 887..481	45-64	431-453	LINAP		g1723476	204	99	2.00E-20	47	57	hypothetical 22.2 KD protein C17G8.03C in chromosome I ; (Z69795) unknown
23616	ENU07410	ANI61C1049 4:3226..2619	116-135	469-488	LINAP		g4493697	43	71	9.00E-12			[Schizosaccharomyces pombe] (Y18863) Pop4 protein [Homo sapiens]
23617	ENU07411	ANI61C5529: 36-55 1940..700	36-55	801-828	LINAP		g2342601	95	59	0.000000			(X89442) peptide synthetase [Metarhizium anisopliae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23618	ENU07412	ANI61C1106 5:6587..6241	37-56	456-475	LINAP		g3219959	211	128	3.00E-29	47	32	"probable zinc metalloproteinase C17A5.04C precursor ; (Z98849) probable zinc metalloproteinase, disintegrin [Schizosaccharomyces pombe] "
23619	ENU07413	ANI61C8968: 932..2028	22-48	809-828	LINAP		g2501739	204	123	1.00E-27	31	19	"putative 151.3 KD transcriptional regulatory protein ; probable membrane protein YLR278c - yeast (Saccharomyces cerevisiae) ; (U17243) Serine, glutamine, asparagine rich central portion of protein [Saccharomyces cerevisiae] "
23620	ENU07414	ANI61C1108: 3803..3001	26-49	760-782	LINAP		g3334796	217	131	5.00E-30	34	52	(AL031107) putative secreted glucosidase [Streptomyces coelicolor] (AB018321) KIAA0778 protein [Homo sapiens]
23621	ENU07415	ANI61C4622: 210..1318	37-57	657-678	LINAP		g3882277	259	112	3.00E-24	37	38	(AL031107) putative secreted glucosidase [Streptomyces coelicolor] (AB018321) KIAA0778 protein [Homo sapiens]
23622	ENU07416	ANI61C5567: 1..1008	22-44	805-829	LINAP		g3560207	275	141	6.00E-33			(AL031536) fnx1p. [Schizosaccharomyces pombe]
23623	ENU07417	ANI61C893:5 964..4504	38-57	800-827	LINAP		g2270900	869	235	2.00E-61	48	97	(U66283) dihydropterolate synthase [Pneumocystis carinii f. sp. muris]
23624	ENU07418	ANI61C1110 3:331..652			LINAP		g4006889	72	49	0.00002	33	32	(Z99708) putative protein [Arabidopsis thaliana]
23625	ENU07419	ANI61C1051 3:446..782	22-43	456-475	LINAP		g2765035	106	69	2.00E-11	38	12	(Y09899) sensory histidine protein kinase [Calothrix viguieri]
23626	ENU07420	ANI61C1111 0:2185..1270	22-49	794-813	LINAP		g3024443	362	149	3.00E-35	34	82	pyrroline-5-carboxylate reductase (P5CR) (P5C reductase) ; pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Zalerion arboricola ; (U33266) pyrroline carboxylate reductase [Zalerion arboricola]
23627	ENU07421	ANI61C1047 7:2007..3198	22-42	809-829	LINAP		g2826168	224	109	2.00E-23	31	64	(AB010714) salicylate hydroxylase [Pseudomonas putida]
23628	ENU07422	ANI61C5574: 2915..3635	23-50	678-699	LINAP		g2661610	436	168	1.00E-43	49	90	(AL009197) hypothetical ubiquitin conjugating enzyme [Schizosaccharomyces pombe]
23629	ENU07423	ANI61C1107 3:2565..3336	25-44	717-736	LINAP		g1673402	118	47	0.000000	30	46	(Z82044) hypothetical 54.4 kd protein [Bacillus subtilis]

Accession

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23630	ENU07424	ANI61C1047 7:9261..10917	22-45	660-679	LINAP		g3023956	1264	282	5.00E-81	54	20	vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospora anserina]
23631	ENU07425	ANI61C558:1 .424	36-63	366-385	LINAP		g1166378	109	66	1.00E-10	34	12	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata] "
23632	ENU07426	ANI61C1107 3:8638..9147	35-54	460-487	LINAP		g1150442	134	81	5.00E-15			"(Z46869) exo-1,3-beta-glucanase/1,3-beta-D-Glucan glucanohydrolase [Kluyveromyces lactis] "
23633	ENU07427	ANI61C1050 9:2651..3170	54-73	387-406	LINAP		g2462678	108	34	0.003	32	40	(Z99568) recombinational dna repair protein rhp55p. [Schizosaccharomyces pombe] ; (AF053410) recombinational DNA repair protein Rhp55p [Schizosaccharomyces pombe]
23634	ENU07428	ANI61C5640: 527..17	22-49	335-357	LINAP		g1352987	275	121	3.00E-27	40	41	BTN1 protein ; probable membrane protein YJL059w - yeast (Saccharomyces cerevisiae) ; (Z49334) ORF YJL059w [Saccharomyces cerevisiae]
23635	ENU07429	ANI61C8997: 48-70 1040..656	48-70	314-333	LINAP		g3901117	193	92	1.00E-18	38	20	(AJ012752) maltose permease [Saccharomyces cerevisiae]
23636	ENU07430	ANI61C4607: 35-55 2725..2293	35-55	426-445	LINAP		g2959337	95	61	0.000000	23	71	(AJ224767) hypothetical protein [Acinetobacter sp. ADP1]
23637	ENU07431	ANI61C5576: 50-69 5415..4439	50-69	799-817	LINAP		g2645229	365	150	9.00E-36	35	49	(U78597) kinesin light chain [Plectonema boryanum]
23638	ENU07432	ANI61C1109 9:2053..2776	38-57	680-703	LINAP		g3184386	149	35	0.66			(AF043102) surface glycoprotein A [Pneumocystis carinii]
23639	ENU07433	ANI61C4629: 22-46 1396..180	22-46	620-643	LINAP		g2414656	613	191	4.00E-48	38	55	(Z99261) putative aminotransferase [Schizosaccharomyces pombe]
23640	ENU07434	ANI61C5639: 87-111 695..384	87-111	308-332	LINAP		g2555098	234	58	0.000000	45	27	(AF019407) GTP-binding protein [Caulobacter crescentus]
23641	ENU07435	ANI61C1109 9:4414..4960	22-40	464-483	LINAP		g3489	204	62	0.000000	36	79	(X03449) unidentified reading frame [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23642	ENU07436	ANI61C1051 5:1440..1	22-47	721-740	LINAP		g2498346	1342	351	4.00E-96	59	44	probable electron transfer flavoprotein-ubiquinone oxidoreductase precursor (ETF-QO) (ETF-ubiquinone oxidoreductase) (ETF dehydrogenase) (electron-transferring-flavoprotein dehydrogenase) ; hypothetical protein YOR356w - yeast (Saccharomyces cerevisiae) ; (Z75264) ORF YOR356w [Saccharomyces cerevisiae]
23643	ENU07437	ANI61C460:5 253..4307	22-48	805-827	LINAP		g2133702	326	93	3.00E-28			phosphorylase kinase (EC 2.7.1.38) gamma chain - fruit fly (Drosophila melanogaster) ; (U13014)
23644	ENU07438	ANI61C4647: 49-67 1379..1	49-67	762-780	LINAP		g3163925	307	114	7.00E-25	29	13	phosphorylase kinase gamma [Drosophila melanogaster]
23645	ENU07439	ANI61C1051 22-42 1:2645..2166	22-42	453-479	LINAP		g2497529	113	65	4.00E-10	38	21	(Y17317) polyketide synthase [Aspergillus fumigatus]
23646	ENU07440	ANI61C8980: 22-45 3812..2877	22-45	776-795	LINAP		g4008344	153	39	0.054			Diatom spindle kinesin 1 ; (U51680) diatom spindle kinesin 1 [Cylindrotheca fusiformis] (Z35639) cDNA EST CEMSD23F comes from this gene; cDNA EST CEESE24F comes from this gene; cDNA EST EMBL:D33683 comes from this gene; cDNA EST EMBL:D36566 comes from this gene; cDNA EST EMBL:D36682 comes from this gene; cDNA EST ... (X69481) GTPase [Saccharomyces cerevisiae]
23647	ENU07441	ANI61C5655: 46-65 636..1524	46-65	625-644	LINAP		g4006	289	129	3.00E-29	32	49	(AC004684) putative ribitol dehydrogenase [Arabidopsis thaliana]
23648	ENU07442	ANI61C1113 23-42 0:977..541	23-42	457-479	LINAP		g3236237	53	47	0.00007			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23649	ENU07443	ANI61C5641: 23-42 2234..1359	23-42	806-828	LINAP		g1175036	188	99	5.00E-20	35	52	"beta-xylosidase (1,4-beta-D-xylan xylohydrolase) (xylan 1,4-beta-xylosidase) / alpha-L-arabinofuranosidase (arabinosidase) ; xylan 1,4-beta-xylosidase (EC 3.2.1.37) - Butyrivibrio fibrisolvens ; (M55537) beta-D-xylosidase/alpha-L-arabinofuranosidase [Butyrivibrio fibrisolvens] "
23650	ENU07444	ANI61C8978: 46-65 1484..1879	46-65	457-479	LINAP		g1377890	65	61	0.000000			(L77083) cdc2 gene product [Nicotiana tabacum]
23651	ENU07445	ANI61C1051: 22-47 1:3430..2845	22-47	532-551	LINAP		g2978452	96	73	2.00E-12			(AE001274) MCAK; L549.3 [Leishmania major]
23652	ENU07446	ANI61C4646: 23-42 3587..2915	23-42	626-652	LINAP		g543754	212	85	4.00E-16	40	29	acetylcholinesterase precursor (ACHE)
23653	ENU07447	ANI61C1110: 34-53 0:3330..2673	34-53	611-630	LINAP		g1352996	184	79	7.00E-20	38	24	hypothetical 68.8 KD protein in EXO70-ARP4 intergenic region ; hypothetical protein YJL083w - yeast (Saccharomyces cerevisiae) ; (X88851) hypothetical protein [Saccharomyces cerevisiae] ; (X83502) J1002 [Saccharomyces cerevisiae] ; (Z49358) ORF YJL083w [Saccharomyces cerevisiae]
23654	ENU07448	ANI61C8986: 22-42 2620..3097	22-42	457-477	LINAP		g731862	82	75	3.00E-13	34	10	"Nucleoporin NUP159 (nuclear pore protein NUP159) ; nucleoporin RAT7 - yeast (Saccharomyces cerevisiae) ; (Z38125) orf, len: 1460,CAI: 0.15 [Saccharomyces cerevisiae] ; (L40634) nucleoporin [Saccharomyces cerevisiae] "
23655	ENU07449	ANI61C1052: 161-182 5:5633..4932	161-182	639-658	LINAP		g1172047	107	79	3.00E-14	34	33	Lyosomal pro-X carboxypeptidase precursor (prolylcarboxypeptidase) (PRCP) (proline carboxypeptidase) (angiotensinase C) (lysosomal carboxypeptidase C) ; lysosomal Pro-X carboxypeptidase (EC 3.4.16.2) - human ; (L13977) prolylcarboxypeptidase [Homo sapiens]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23656	ENU07450	ANI61C5629: 23-43 3467..1943	23-43	806-828	LINAP		g3121733	1250	243	2.00E-66	56	34	"aconitate hydratase, mitochondrial precursor (citrate hydro-lyase) (aconitase) ; (Z98601) aconitate hydratase. [Schizosaccharomyces pombe]"
23657	ENU07451	ANI61C1055: 22-43 871..104	22-43	580-602	LINAP		g3925783	538	237	6.00E-62	52	55	(AL034353) glutamate n-acetyltransferase precursor [Schizosaccharomyces pombe]
23658	ENU07452	ANI61C459:1 27-46 002..1	27-46	801-828	LINAP		g2119802	366	105	4.00E-36	37	40	probable membrane protein YDL247w - yeast (Saccharomyces cerevisiae) ; (Z74295) ORF YDL247w [Saccharomyces cerevisiae]
23659	ENU07453	ANI61C9012: 22-47 1882..1172	22-47	665-684	LINAP		g541082	164	77	1.00E-13	36	63	GutQ homolog - Escherichia coli
23660	ENU07454	ANI61C1116 197-216 3:4552..3479	197-216	777-796	LINAP		g3738162	549	203	1.00E-51	49	53	(AL031856) putative involvement in protein glycosylation in the golgi [Schizosaccharomyces pombe]
23661	ENU07455	ANI61C1054 23-43 5:677..283	23-43	413-432	LINAP		g2494853	43	59	0.000000			probable hydroxyacylglutathione hydrolase (glyoxalase II) (GLX II) ; (D83536) unknown [Escherichia coli] ; (U70214) hypothetical protein [Escherichia coli] ; (AE000130) probable hydroxyacylglutathione hydrolase [Escherichia coli]
23662	ENU07456	ANI61C4681: 49-73 1354..669	49-73	524-546	LINAP		g4514622	222	109	2.00E-23	37	61	(AB011211) pectin methylesterase [Aspergillus oryzae]
23663	ENU07457	ANI61C9019: 22-49 1260..397	22-49	690-714	LINAP		g3560143	481	198	3.00E-51	58	42	(AL031534) putative vacuolar protein sorting-associated protein [Schizosaccharomyces pombe]
23664	ENU07458	ANI61C1115: 59-81 1340..3049	59-81	808-829	LINAP		g1346099	1100	197	8.00E-50	47	45	Glycolipid anchored surface protein precursor (glycoprotein GP115) ; glycopospholipid-anchored surface glycoprotein GAS1 precursor - yeast (Saccharomyces cerevisiae) ; (X56399) glycoprotein gp115 [Saccharomyces cerevisiae] ; (Z49212) Gas1p [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23665	ENU07459	ANI61C4696: 1134..477	101-123	612-637	LINAP		g731945	129	80	1.00E-14	30	23	putative 86.7 KD transcriptional regulatory protein in NUC1-NCE1 intergenic region ; finger protein YJL206c - yeast (Saccharomyces cerevisiae) ; (X77688) hypothetical protein J0316 [Saccharomyces cerevisiae] ; (Z49481) ORF YJL206c [Saccharomyces cerevisiae]
23666	ENU07460	ANI61C4709: 532..1			LINAP		g1705462	125	68	6.00E-12	37	26	"adenosylmethionine-8-amino-7-oxonanoate aminotransferase (7,8-diamino-pelargonic acid aminotransferase) (DAPA aminotransferase) ; BIO3 protein - yeast (Saccharomyces cerevisiae) ; (Z71673) ORF YNR058w [Saccharomyces cerevisiae] "
23667	ENU07461	ANI61C5635: 1715..495	43-70	794-817	LINAP		g1084961	197	41	7.00E-11			lipase - yeast (Geotrichum candidum) ; (U02387) lipase [Geotrichum candidum] ; lipase I [Galactomyces geotrichum]
23668	ENU07462	ANI61C1050 5:9182..10097	27-54	809-828	LINAP		g3915140	306	78	1.00E-13	32	37	isotrichodermin C-15 hydroxylase (cytochrome P450 65A1) ; (AF011355) isotrichodermin C-15 hydroxylase [Fusarium sporotrichioides]
23669	ENU07463	ANI61C464:4 64..1102	48-67	577-596	LINAP		g130784	68	72	4.00E-12			Pyrimidine pathway regulatory protein 1 ; regulatory protein PPR1 - yeast (Saccharomyces cerevisiae) ; (X01739) regulatory protein (AA 1-904) [Saccharomyces cerevisiae] ; (Z73186) ORF YLR014c [Saccharomyces cerevisiae]
23670	ENU07464	ANI61C464:5 802..6738	44-71	805-829	LINAP		g1171129	104	81	9.00E-15	25	10	(U24657) saframycin Mx1 synthetase A [Myxococcus xanthus]
23671	ENU07465	ANI61C1476: 2762..1351	22-41	805-823	LINAP		g4507551	177	76	3.00E-13	32	16	transmembrane protein 1 ; epilepsy holoprosencephaly candidate-1 protein (EHOC-1) (transmembrane protein 1) ; probable transmembrane protein - human ; (U19252) putative transmembrane protein [Homo sapiens]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23672	ENU07466	ANI61C9001: 38-64 3362..1	38-64	804-828	LINAP		g1834342	3543	329	e-119	76	19	(Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
23673	ENU07467	ANI61C1476: 5187..4809			LINAP		g3859670	154	82	2.00E-15	38	19	(AL033502) hypothetical membrane protein [Candida albicans]
23674	ENU07468	ANI61C5635: 66-85 4748..4091	66-85	614-637	LINAP		g544191	144	67	3.00E-18	41	25	protein kinase DSK1 (DIS1-suppressing protein kinase) ; dis1-suppressing protein kinase dsk1 - fission yeast (Schizosaccharomyces pombe) ; (D13447) protein kinase [Schizosaccharomyces pombe]
23675	ENU07469	ANI61C1115 49-68 7:5462..5836	49-68	458-479	LINAP		g417770	328	143	1.00E-33	45	21	zinc finger protein SFP1 ; split zinc finger protein 1 - yeast (Saccharomyces cerevisiae) ; (U19729) Sfp1p [Saccharomyces cerevisiae]
23676	ENU07470	ANI61C9031: 30-50 1..938	30-50	806-829	LINAP		g544368	189	91	1.00E-19	29	54	Galactose-proton symport (galactose transporter) ; (U28377) ORF_0464 [Escherichia coli] ; (AE000377) galactose-proton symport of transport system [Escherichia coli]
23677	ENU07471	ANI61C1571: 22-49 637..1	22-49	510-536	LINAP		g3006192	649	200	6.00E-51	58	39	(AL022304) putative galactosyltransferase associated protein kinase [Schizosaccharomyces pombe]
23678	ENU07472	ANI61C4717: 22-48 260..1027	22-48	724-744	LINAP		g2133011	318	99	4.00E-20	45	39	probable membrane protein YPL260w - yeast (Saccharomyces cerevisiae) ; (Z73617) ORF YPL260w [Saccharomyces cerevisiae]
23679	ENU07473	ANI61C5710: 38-57 1706..2075	38-57	426-445	LINAP		g2808753	206	115	3.00E-25	38	7	(AL021409) polyketide synthase [Streptomyces coelicolor]
23680	ENU07474	ANI61C904:5 55-74 30..1	55-74	395-414	LINAP		g1723926	298	115	3.00E-25	48	18	"hypothetical 78.1 KD protein in TIP20-MRF1 intergenic region ; hypothetical protein YGL144c - yeast (Saccharomyces cerevisiae) ; (Z72666) ORF YGL144c [Saccharomyces cerevisiae] ; (X99960) putative, YGL144c [Saccharomyces cerevisiae] "

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23681	ENU07475	ANI61C1578: 1..419	22-45	358-377	LINAP		g134968	320	152	9.00E-37	54	25	serine/threonine protein kinase STE7 ; regulatory protein STE7 - yeast (Saccharomyces cerevisiae) ; (M14097) STE7 protein [Saccharomyces cerevisiae] ; (Z67750) regulatory protein STE7 [Saccharomyces cerevisiae] ; (Z74207) ORF YDL159w [Saccharomyces cerevisiae] probable membrane protein YOR320c - yeast (Saccharomyces cerevisiae) ; (X90565) orf 06145 [Saccharomyces cerevisiae] ; (Z75228) ORF YOR320c [Saccharomyces cerevisiae] (AB014885) HrPOPK-1 [Halocynthia roretzi] hypothetical 89.2 KD protein in RARI-SCJ1 intergenic region ; probable membrane protein YMR212c - yeast (Saccharomyces cerevisiae) ; (Z49809) unknown [Saccharomyces cerevisiae] (AB007927) KIAA0458 protein [Homo sapiens] "glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) ; (Z38061) mal5, sta1, len: 1367, CAI: 0.3, AMYH_YEAST P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae] ; (U30626) glucoamylase [Saccharomyces cerevisiae var. diastaticus] " glycoprotein GP100 precursor (P29F8) ; (L04286) glycoprotein gp100 [Dictyostelium discoideum] (AF059534) severin kinase [Dictyostelium discoideum]
23682	ENU07476	ANI61C9003: 763..247	22-48	448-467	LINAP		g2132946	156	89	3.00E-17	35	29	
23683	ENU07477	ANI61C1555: 1..1288	22-47	805-824	LINAP		g3172111	657	185	3.00E-46	43	30	
23684	ENU07478	ANI61C1118: 8:5374..3784	29-56	803-829	LINAP		g2497190	175	38	0.07			
23685	ENU07479	ANI61C4702: 1643..1059	22-47	532-551	LINAP		g3413878	110	37	0.001			
23686	ENU07480	ANI61C9003: 5306..7862	22-43	809-828	LINAP		g728850	574	40	0.024			
23687	ENU07481	ANI61C1598: 800..468	122-141	285-304	LINAP		g544411	71	45	0.0002			
23688	ENU07482	ANI61C1057: 8:603..1764	22-44	805-824	LINAP		g3075511	342	104	2.00E-26	37	45	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23689	ENU07483	ANI61C4702: 25-48 3622..3185	25-48	452-479	LINAP		g4499843	131	55	0.000000	34	30	(AJ011965) oxidoreductase [Claviceps purpurea]
23690	ENU07484	ANI61C1120 22-47 2:242..1069	22-47	752-771	LINAP		g732206	394	101	9.00E-21	41	78	Autophagocytosis protein AUT1 ; hypothetical protein YNR007c - yeast (Saccharomyces cerevisiae) ; (X77395) N2040 [Saccharomyces cerevisiae] ; (Z71622) ORF YNR007c [Saccharomyces cerevisiae]
23691	ENU07485	ANI61C1059 4:1..1061			LINAP		g1723076	321	71	2.00E-26	35	46	hypothetical 57.3 KD protein GMC-type oxidoreductase CY50.03C ; (Z77137) hypothetical protein Rv1279 [Mycobacterium tuberculosis]
23692	ENU07486	ANI61C4730: 22-41 953..1	22-41	743-764	LINAP		g2133023	495	208	4.00E-53	39	32	probable membrane protein YPR091c - yeast (Saccharomyces cerevisiae) ; (U51033) Similar in central region to C. elegans hypothetical protein F55C12.5 (GenBank accession number U41107) [Saccharomyces cerevisiae]
23693	ENU07487	ANI61C9036: 25-44 3594..2846	25-44	708-728	LINAP		g4585623	183	39	0.046			(AJ133651) conidiospore surface protein [Trichoderma harzianum]
23694	ENU07488	ANI61C16:29 5..1437	122-141	744-763	LINAP		g3172113	1741	559	e-159	95	17	(AB014886) typeII DNA topoisomerase [Emericella nidulans]
23695	ENU07489	ANI61C1059 68-87 3:1..1731	68-87	764-784	LINAP		g3821332	240	98	8.00E-20	29	25	(AL033127) hypothetical protein [Schizosaccharomyces pombe]
23696	ENU07490	ANI61C5643: 22-48 4851..4395	22-48	452-479	LINAP		g465491	261	68	2.00E-26	46	30	"beta-xylosidase (1,4-beta-D-xylan xylohydrolase) (xylan 1,4-beta-xylosidase) ; xylan 1,4-beta-xylosidase (EC 3.2.1.37) - Bacillus pumilus ; (X05793) xylan 1,4-beta-xylosidase [Bacillus pumilus] "
23697	ENU07491	ANI61C1118 22-47 3:5396..7922	22-47	777-795	LINAP		g2613108	2260	345	e-104	65	24	(AF030554) class V chitin synthase [Ustilago maydis]
23698	ENU07492	ANI61C57:41 22-45 8..2193	22-45	808-828	LINAP		g710551	163	78	1.00E-13			(L40632) ankyrin 3 [Mus musculus]
23699	ENU07493	ANI61C1120 54-72 3:4450..3389	54-72	786-813	LINAP		g1635521	200	103	1.00E-21	27	51	(D90914) beta-glucosidase [Synechocystis sp.]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23700	ENU07494	ANI61C1059 8:2380..882	22-43	807-829	LINAP		g549643	775	161	1.00E-49	43	29	hypothetical 102.7 KD protein in PRP16-SRP40 intergenic region ; hypothetical protein YKR089c - yeast (Saccharomyces cerevisiae) ; (Z27116) ORF YKR409 [Saccharomyces cerevisiae] ; (Z28314) ORF YKR089c [Saccharomyces cerevisiae] (M94916) ubiquitin-specific processing protease [Saccharomyces cerevisiae] delta-1-pyrroline-5-carboxylate dehydrogenase precursor (P5C dehydrogenase) ; (X95584) 1-pyrroline-5-carboxylate dehydrogenase [Agaricus bisporus] (AF107264) glutamate synthase large subunit [Rhizobium etli] Metal homeostasis protein BSD2 ; metal homeostasis protein BSD2 - yeast (Saccharomyces cerevisiae) ; (X76053) YBR2037-ORF [Saccharomyces cerevisiae] ; (L33783) metal homeostasis protein [Saccharomyces cerevisiae] ; (Z36159) ORF YBR290w [Saccharomyces cerevisiae] ; ORF YBR2037 [Saccharomyces cerevisiae] (AL035247) ion transporter [Schizosaccharomyces pombe] pol polyprotein - fruit fly (Drosophila melanogaster) transposon 1731 ; (X07656) pol polypeptide (AA 1-982) [Drosophila melanogaster] hypothetical 47.8 KD protein in HSP26-TIF32 intergenic region ; aminopeptidase Y homolog - yeast (Saccharomyces cerevisiae) ; (X76294) ORF YBRO718 [Saccharomyces cerevisiae] ; (Z35943) ORF YBR074w [Saccharomyces cerevisiae]
23701	ENU07495	ANI61C465:2 478..4468	22-49	804-829	LINAP		g173128	510	123	1.00E-27			
23702	ENU07496	ANI61C5689: 40-59 3897..4786	40-59	730-754	LINAP		g2494072	558	150	7.00E-57	48	46	
23703	ENU07497	ANI61C1060 0:2213..2711	36-55	367-387	LINAP		g4038458	230	53	1.00E-14	45	7	
23704	ENU07498	ANI61C465:9 120..9481	64-83	453-479	LINAP		g586358	172	72	2.00E-15			
23705	ENU07499	ANI61C1058 6:2054..1345	29-47	668-688	LINAP		g4164420	644	117	9.00E-26	41	59	
23706	ENU07500	ANI61C4751: 34-53 871..1704	34-53	749-773	LINAP		g85105	316	101	5.00E-21	39	13	
23707	ENU07501	ANI61C6475: 22-49 1453..2048	22-49	419-438	LINAP		g586511	187	99	6.00E-22	41	43	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23708	ENU07502	ANI61C9037: 22-45 1753..1442	457-476	457-476	LINAP	Database Hit	g3879015	95	52	0.000003	39	100	"(Z81108) similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL:D73942 comes from this gene; cDNA EST yk257f10.5 comes from this gene; cDNA EST EMBL:D70930 comes from this gene; cDNA EST EMBL:D73476 come..."
23709	ENU07503	ANI61C1611: 46-65 1330..376	725-746	725-746	LINAP		g2131263	873	196	1.00E-77	65	11	GLT1 protein - yeast (Saccharomyces cerevisiae) ; (Z67750) putative protein [Saccharomyces cerevisiae] ; (Z74219) ORF YDL171c [Saccharomyces cerevisiae]
23710	ENU07504	ANI61C6464: 36-54 666..332	456-479	456-479	LINAP		g557084	38	55	0.000000	2		(L35601) ankyrin [Drosophila melanogaster] ; ankyrin [Drosophila melanogaster]
23711	ENU07505	ANI61C9056: 97-116 2136..1496	595-620	595-620	LINAP		g3581879	366	116	1.00E-25	43	21	(AL031540) hypothetical ATP binding protein [Schizosaccharomyces pombe]
23712	ENU07506	ANI61C1557: 22-47 4403..2640	802-829	802-829	LINAP		g116453	720	36	0.35			"sodium channel protein, skeletal muscle alpha-subunit (MU-1) ; sodium channel protein mu1 alpha chain, skeletal muscle - rat ; (M26643) voltage-sensitive sodium channel alpha subunit [Rattus norvegicus] "
23713	ENU07507	ANI61C5732: 22-46 516..1	386-413	386-413	LINAP		g1351672	106	65	3.00E-10	28	16	putative 89.3 KD transcriptional regulatory protein C1F7.11C ; hypothetical protein SPAC1F7.11c - fission yeast (Schizosaccharomyces pombe) ; (Z67998) unknown
23714	ENU07508	ANI61C6469: 41-60 1051..174	803-829	803-829	LINAP		g2612904	322	109	2.00E-23	35	79	[Schizosaccharomyces pombe] (AF015825) malate dehydrogenase-like protein [Bacillus subtilis] ; (Z99110) similar to malate dehydrogenase [Bacillus subtilis]
23715	ENU07509	ANI61C1619: 48-69 648..1090	459-478	459-478	LINAP		g4519535	217	91	4.00E-18	34	31	(AB015306) Leukotriene B4 omega-hydroxylase [Homo sapiens]
23716	ENU07510	ANI61C567:1 32-51 213..866	456-479	456-479	LINAP		g3319757	64	58	0.000000	33	13	(AL031035) putative ATP/GTP-binding protein [Streptomyces coelicolor]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23717	ENU07511	ANI61C6430: 6653..6314	30-51	443-470	LINAP		g3257375	91	37	0.08			(AP000004) 275aa long hypothetical translation initiation factor eIF-2 alpha chain [Pyrococcus horikoshii]
23718	ENU07512	ANI61C9058: 1..509	57-76	458-477	LINAP		g1351343	48	75	3.00E-13	28	15	positive regulator of purine utilisation ; positive regulator of purine utilisation - Emericella nidulans ; (X84015)
23719	ENU07513	ANI61C568:2 880..3595	22-48	670-695	LINAP		g127338	149	48	4.00E-11	30	18	positive regulator of purine utilisation [Emericella nidulans] morphogenesis-related protein (multicopy suppression of a budding defect 1) ; morphogenesis-related protein MSB1 - yeast (Saccharomyces cerevisiae) ; (M37767) multicopy suppressor of a budding defect [Saccharomyces cerevisiae] ; (Z75096) ORF YOR188w [Saccharomyces cerevisiae]
23720	ENU07514	ANI61C9070: 1118..1			LINAP		g2832315	1046	356	e-101	69	38	(AF045014) translation release factor eRF3 [Podospora anserina]
23721	ENU07515	ANI61C1617: 1583..2072	25-52	457-479	LINAP		g1834342	439	154	4.00E-37	66	10	(Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
23722	ENU07516	ANI61C4767: 318..1	102-127	453-479	LINAP		g3913990	57	50	0.00001	29	14	ATP-dependent protease LA ; (AF030688) ATP-dependent proteinase [Mycobacterium smegmatis]
23723	ENU07517	ANI61C568:7 265..6706	28-47	502-528	LINAP		g2981452	299	127	6.00E-29	45	91	(AF052482) germinating protein [Erysiphe graminis]
23724	ENU07518	ANI61C6462: 4185..3107	70-89	804-829	LINAP		g134388	373	91	1.00E-35	42	78	L-serine dehydratase (L-serine deaminase) ; L-serine dehydratase (EC 4.2.1.13) SDL1 - yeast (Saccharomyces cerevisiae) ; (X52657) L-serine dehydratase (AA 1-338)
23725	ENU07519	ANI61C9042: 1623..912	22-41	646-665	LINAP		g4499843	270	83	2.00E-15	42	40	[Saccharomyces cerevisiae] (AJ011965) oxidoreductase [Claviceps purpurea]
23726	ENU07520	ANI61C1628: 2453..2797	25-50	331-350	LINAP		g98686	28	49	0.00002			internalin B - Listeria monocytogenes

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23727	ENU07521	ANI61C1060 4:1987..1325	24-51	611-629	LINAP		g3924850	99	59	2.00E-14			"(Z81586) predicted using Genefinder; similar to Alcohol/other dehydrogenases, short chain type [Caenorhabditis elegans] "
23728	ENU07522	ANI61C4780: 94..516	54-81	451-470	LINAP		g3873652	112	73	1.00E-12			(Z71177) Similarity with human nuclear autoantigen (PIR accession number JC2522); cDNA EST EMBL:D65093 comes from this gene; cDNA EST EMBL:D68406 comes from this gene; cDNA EST yk297d9.5 comes from this gene; cDNA EST yk353f10... ; (Z71181) Similarity with human nuclear autoantigen (PIR accession number JC2522); cDNA EST EMBL:D65093 comes from this gene; cDNA EST EMBL:D68406 comes from this gene; cDNA EST yk297d9.5 comes from this gene; cDNA EST yk353f10...
23729	ENU07523	ANI61C5751: 1204..1	31-50	721-740	LINAP		g2440206	1023	272	3.00E-72	51	36	(Z99532) putative integral membrane protein [Schizosaccharomyces pombe]
23730	ENU07524	ANI61C6462: 5222..5951	22-49	685-709	LINAP		g1351719	102	61	0.000000	34	71	hypothetical 30.0 KD protein C18G6.01C in chromosome I ; (Z68198) hypothetical protein [Schizosaccharomyces pombe]
23731	ENU07525	ANI61C9042: 5892..5338			LINAP		g114959	220	87	6.00E-21	40	22	Thermostable beta-glucosidase B (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) ; beta-glucosidase (EC 3.2.1.21) B - Clostridium thermocellum ; (X15644) bglB gene (AA1-754) [Clostridium thermocellum]
23732	ENU07526	ANI61C1062 1:1..406	22-46	346-365	LINAP		g710552	126	75	2.00E-13	40	6	(L40632) ankyrin 3 [Mus musculus]
23733	ENU07527	ANI61C4785: 764..1211	22-48	444-463	LINAP		g1546072	248	52	2.00E-13	40	5	(U68040) polyketide synthase [Cochliobolus heterostrophus]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23734	ENU07528	ANI61C6502: 22-47 240..779	22-47	422-448	LINAP	LINAP	g2132816	256	130	8.00E-30	38	53	probable membrane protein YOL002c - yeast (Saccharomyces cerevisiae) ; (U43491) hypothetical protein UND327 [Saccharomyces cerevisiae] ; (Z74744) ORF YOL002c [Saccharomyces cerevisiae]
23735	ENU07529	ANI61C4789: 1093..1483			LINAP			30				29	
23736	ENU07530	ANI61C5728: 1182..1849			LINAP		g729781	159	45	0.000000			probable glucoSE transporter HXT5 ; hexose transport protein HXT5 - yeast (Saccharomyces cerevisiae) ; (X77961) hexose transporter [Saccharomyces cerevisiae] ; (U00060) Hxt5p: Hexose transporter [Saccharomyces cerevisiae] A-aggutinin attachment subunit precursor ; a-aggutinin core protein AGA1 - yeast (Saccharomyces cerevisiae) ; (M60590) a-aggutinin core subunit [Saccharomyces cerevisiae] ; (Z71659) ORF YNR044w [Saccharomyces cerevisiae] (AF009417) cytochrome P450 [Myrothecium rostratum] (Z97052) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein MJ0301 ; hypothetical protein MJ0301 - Methanococcus jannaschii ; (U67485) conserved hypothetical protein [Methanococcus jannaschii] (L35053) endonuclease [Magnaporthe grisea]
23737	ENU07531	ANI61C6472: 82-108 2582..2106	82-108	452-479	LINAP		g416592	101	42	0.003			general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) ; (Z73074) ORF YGR289c [Saccharomyces cerevisiae]
23738	ENU07532	ANI61C907:8 45-71 2..1854	45-71	807-829	LINAP		g2267601	474	109	2.00E-23	39	39	
23739	ENU07533	ANI61C1652: 57-74 1249..2315	57-74	720-741	LINAP		g2213557	682	176	2.00E-43	40	52	
23740	ENU07534	ANI61C1060 40-62 3-4136..3828	40-62	450-477	LINAP		g2495901	124	69	2.00E-11	32	34	
23741	ENU07535	ANI61C5782: 179-206 1..1467	179-206	673-700	LINAP		g522302	755	219	2.00E-56	44	23	
23742	ENU07536	ANI61C6429: 37-56 4404..2930	37-56	789-808	LINAP		g1703215	74	80	2.00E-14			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23743	ENU07537	ANI61C9091: 26-47 1571..756	26-47	757-776	LINAP		g2494090	174	82	6.00E-15	27	86	hypothetical 33.3 KD protein in PERR-ARGF intergenic region ; (AE000134) putative lyase/synthase [Escherichia coli]
23744	ENU07538	ANI61C1675: 47-66 1739..2203	47-66	431-454	LINAP		g1723643	355	153	7.00E-37	52	37	hypothetical 44.9 KD protein in SEC9-MSB2 intergenic region ; probable membrane protein YGR010w - yeast (Saccharomyces cerevisiae) ; (Z72795) ORF YGR010w [Saccharomyces cerevisiae]
23745	ENU07539	ANI61C1061 22-49 4:2063..3065	22-49	774-797	LINAP		g3757672	148	70	2.00E-11	25	26	(AJ010902) inversin [Mus musculus]
23746	ENU07540	ANI61C4814: 104-125 694..1	104-125	558-576	LINAP		g2920706	498	242	3.00E-63	51	28	(Y13568) beta-xylosidase [Emericella nidulans]
23747	ENU07541	ANI61C4817: 71-90 1225..914	71-90	438-457	LINAP		g3413872	168	33	1.6			(AB007924) KIAA0455 protein [Homo sapiens]
23748	ENU07542	ANI61C566:6 106-133 860..7865	106-133	796-823	LINAP		g1363735	84	32	5.3			probable membrane protein YLR242c - yeast (Saccharomyces cerevisiae) ; (U20865) Arv1p [Saccharomyces cerevisiae]
23749	ENU07543	ANI61C4815: 32-52 1691..415	32-52	806-829	LINAP		g549443	547	210	1.00E-53	37	14	conidial green pigment synthase ; probable polyketide synthase - Emericella nidulans ; (X65866) putative polyketide or fatty acid synthase [Emericella nidulans] ; wA gene [Emericella nidulans]
23750	ENU07544	ANI61C1062 22-48 2:4990..5304	22-48	458-479	LINAP		g465533	166	36	0.14			hypothetical 11.5 KD protein in HTB2-NTH2 intergenic region ; hypothetical protein YBL001c - yeast (Saccharomyces cerevisiae) ; (Z26494) unknown [Saccharomyces cerevisiae] ; (Z35762) ORF YBL001c [Saccharomyces cerevisiae] ; ORF YBL0105 [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23751	ENU07545	ANI61C9597: 46-72 848..1	712-738	712-738	LINAP	Database Hit	g4505499	421	148	6.00E-35	38	25	O-GlcNAc transferase (uridine diphospho-N-acetylglucosamine:polypeptide beta-N-acetylglucosaminyl transferase) ; (U77413) O-linked GlcNAc transferase [Homo sapiens]
23752	ENU07546	ANI61C9593: 22-44 2213..3056	779-806	779-806	LINAP		g2133786	89	39	0.053			NF-180 - sea lamprey ; (U19361) NF-180 [Petromyzon marinus]
23753	ENU07547	ANI61C6503: 57-76 2076..449	615-637	615-637	LINAP		g1077259	837	171	6.00E-42	39	23	probable membrane protein YPL006w - yeast (Saccharomyces cerevisiae) ; (Z48483) unknown [Saccharomyces cerevisiae] ; (U33335) Lpa1lp [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]
23754	ENU07548	ANI61C1674: 22-48 892..300	529-548	529-548	LINAP		g2498563	280	139	2.00E-32	53	46	MLO2 protein ; (L42550) ORF [Schizosaccharomyces pombe]
23755	ENU07549	ANI61C9034: 25-52 4999..5519	480-499	480-499	LINAP		g2689471	95	85	2.00E-16	37	30	(U62774) cytochrome P450 monooxygenase [Aspergillus parasiticus]
23756	ENU07550	ANI61C650:2 080..2671			LINAP		g3150139	108	66	2.00E-10	32	22	(AL023594) amino-acid permease [Schizosaccharomyces pombe]
23757	ENU07551	ANI61C909:4 71..1308	28-47	793-817	LINAP		g1437475	315	106	2.00E-34	33	80	"(D86544) hydroxyquinol-1, 2-dioxygenase [Ralstonia pickettii] "
23758	ENU07552	ANI61C9556: 59-78 1162..1997	59-78	795-814	LINAP		g171963	293	162	4.00E-39	41	53	(M15991) tRNA isopentenyl transferase [Saccharomyces cerevisiae]
23759	ENU07553	ANI61C5675: 40-59 6149..4744	40-59	809-828	LINAP		g1546072	394	63	3.00E-22	41	10	(U68040) polyketide synthase [Cochliobolus heterostrophus]
23760	ENU07554	ANI61C1122 8:6103..6779	26-45	635-656	LINAP		g2497056	85	55	0.000000	30	35	putative dioxygenase YLL057C ; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae) ; (Z47973) ORF L0572 [Saccharomyces cerevisiae] ; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]
23761	ENU07555	ANI61C9102: 22-42 1863..942	22-42	800-819	LINAP		g3036840	378	106	3.00E-22	39	67	(AJ222967) cystinosin [Homo sapiens] ; (Y15924) cystinosin [Homo sapiens]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23762	ENU07556	ANI61C9556: 23-47 3868..3127	23-47	694-721	LINAP		g1723981	296	59	6.00E-13	32	53	hypothetical 44.5 KD protein in PDE1-RTF1 intergenic region ; hypothetical protein YGL246c - yeast (Saccharomyces cerevisiae) ; (X94357) ORF NRE387 [Saccharomyces cerevisiae] ; (Z72768) ORF YGL246c [Saccharomyces cerevisiae] (AL0233587) putative kinesin-like protein [Schizosaccharomyces pombe] ; quinate permease (quininate transporter) ; quinate transport protein - Emericella nidulans ; (X13525) quinate permease [Emericella nidulans] "probable calcium-transporting ATPase 3 (endoplasmic reticulum CA2+-ATPase) ; probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) ; (L01795) ATPase [Saccharomyces cerevisiae] ; (U12980) Drs2p: Membrane spanning Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae] "
23763	ENU07557	ANI61C6476: 22-49 4571..5242	22-49	627-651	LINAP		g3136023	469	168	2.00E-48	54	26	Start control protein CDC10 ; cdc10 start control protein - fission yeast (Schizosaccharomyces pombe) ; (X02175) cdc10 polypeptide [Schizosaccharomyces pombe] (U78597) kinesin light chain [Plectonema boryanum] (AL031798) putative leucine permease transcriptional regulator. [Schizosaccharomyces pombe] (AB018344) KIAA0801 protein [Homo sapiens] (AF102265) N-acetylglucosamine-phosphate mutase [Homo sapiens]
23764	ENU07558	ANI61C1685: 22-47 298..1945	22-47	806-828	LINAP		g131768	381	128	4.00E-29			
23765	ENU07559	ANI61C1127 25-44 6:342..642	25-44	439-466	LINAP		g728905	304	140	7.00E-33	63	7	
23766	ENU07560	ANI61C5756: 66-85 2056..3660	66-85	805-823	LINAP		g115906	375	135	3.00E-31	35	34	
23767	ENU07561	ANI61C1127 29-51 1:669..1	29-51	610-637	LINAP		g2645229	225	85	6.00E-16	29	45	
23768	ENU07562	ANI61C9579: 22-47 6751..5631	22-47	808-829	LINAP		g3687460	402	157	7.00E-38	40	25	
23769	ENU07563	ANI61C65:35 33-52 11..4969	33-52	721-748	LINAP		g3882323	1206	386	e-106	69	26	
23770	ENU07564	ANI61C5811: 22-47 646..1	22-47	546-573	LINAP		g3851711	286	119	2.00E-26	44	32	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23771	ENU07565	ANI61C1123 1:338..1	52-74	439-458	LINAP		g131768	87	61	6.00E-10	31	31	quininate permease (quininate transporter) ; quininate transport protein - Emericella nidulans ; (X13525) quininate permease [Emericella nidulans]
23772	ENU07566	ANI61C5803: 312..1387	22-48	767-786	LINAP		g2500587	621	100	4.00E-30	47	51	Spliceosome associated protein 49 (SAP 49) (SF3B53) ; spliceosome-associated protein SAP-49 - human ; (L35013) spliceosomal protein [Homo sapiens]
23773	ENU07567	ANI61C1703: 38-57 1542..994	38-57	506-525	LINAP		g2132865	170	58	0.000000 06			probable membrane protein YOR034c - yeast (Saccharomyces cerevisiae) ; (X87331) AKR1 homologue; overlaps with L31407 [Saccharomyces cerevisiae] ; (Z74942) ORF YOR034c [Saccharomyces cerevisiae] (AJ223459) Pm1A protein [Emericella nidulans]
23774	ENU07568	ANI61C1123 1:2054..1750	22-43	455-479	LINAP		g2808662	42	55	0.000000 4			hypothetical protein YOR049c - yeast (Saccharomyces cerevisiae) ; (Z74957) ORF YOR049c [Saccharomyces cerevisiae]
23775	ENU07569	ANI61C9063: 22-44 8556..7615	22-44	810-829	LINAP		g2132036	104	106	1.00E-24			alpha-glucosidase precursor (maltase) ; alpha-glucosidase (EC 3.2.1.20) - barley ; (U22450) alpha-glucosidase [Hordeum vulgare]
23776	ENU07570	ANI61C4823: 22-48 4928..3780	22-48	810-829	LINAP		g3023275	926	107	1.00E-42	41	27	"Immunoglobulin G binding protein H precursor (protein H) ; protein H precursor - Streptococcus sp. (group A, strain 40/58) ; (M29398) protein H precursor [Streptococcus sp.] "
23777	ENU07571	ANI61C9110: 22-45 1874..1306	22-45	526-548	LINAP		g1711494	65	37	0.095			(U24215) HOMODA hydrolase [Pseudomonas putida] ; HOMODA hydrolase [Pseudomonas putida]
23778	ENU07572	ANI61C9578: 23-45 4522..4933	23-45	458-479	LINAP		g1263187	72	46	0.0002	26	46	multidrug resistance protein 2 (P-glycoprotein 2) ; multidrug resistance protein 2 - mouse ; (J03398) multidrug resistance protein [Mus musculus]
23779	ENU07573	ANI61C4906: 22-45 2268..1	22-45	726-749	LINAP		g126929	745	139	3.00E-33	48	12	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi g2281979	aat Score 117	Blast Score 50	Blast Prob 0.000006	% id cvrg	Description (Z98056) putative glyoxylate pathway regulator [Schizosaccharomyces pombe]
23780	ENU07574	ANI61C1715: 1..354	114-133	312-332	LINAP							
23781	ENU07575	ANI61C9108: 3744..2763	22-47	807-826	LINAP		g1805251	914	339	1.00E-92	55	51 (U58946) transposase [Aspergillus awamori]
23782	ENU07576	ANI61C5784: 3592..3988	22-45	455-479	LINAP		g4165298	85	56	0.000000	28	20 (AL035254) putative transcriptional regulator [Schizosaccharomyces pombe]
23783	ENU07577	ANI61C4909: 1329..2684	23-43	787-806	LINAP		g3913676	405	143	2.00E-33	32	42 Ferric reductase transmembrane component 7 precursor ; probable membrane protein YOL152w - yeast (Saccharomyces cerevisiae) ; (Z48239)
23784	ENU07578	ANI61C1127 5:1524..1185	22-48	297-319	LINAP		g4468913	210	95	1.00E-19	41	14 orf1 [Saccharomyces cerevisiae] ; (Z74894) ORF YOL152w [Saccharomyces cerevisiae] (AJ131720) alpha integrin binding protein 80 [Homo sapiens]
23785	ENU07579	ANI61C1709: 1..367	102-123	319-346	LINAP		g769829	143	63	9.00E-10	49	14 (M80674) hydroxylase [Streptomyces glaucescens]
23786	ENU07580	ANI61C5854: 1..1173	23-46	803-829	LINAP		g3242253	494	181	6.00E-45	39	11 (Z83857) ppsC [Mycobacterium tuberculosis]
23787	ENU07581	ANI61C1127 8:607..1	53-72	398-420	LINAP		g3025210	85	46	0.0003		"hypothetical 43.0 KD protein in cut-
23788	ENU07582	ANI61C4930: 989..1	32-51	714-741	LINAP		g4467980	127	34	1.8		GLNX intergenic region ; (AE000170) orf, hypothetical protein [Escherichia coli] ; (D90706) VisC protein [Escherichia coli] "
23789	ENU07583	ANI61C1127: 2453..3163	32-51	651-670	LINAP		g3875304	370	164	8.00E-40	42	65 (AJ133272) atrophin-1 [Pongo pygmaeus] (Z74030) predicted using Genefinder; cDNA EST EMBL:C07609 comes from this gene; cDNA EST EMBL:C09023 comes from this gene; cDNA EST yk505e9.3 comes from this gene; cDNA EST yk489h9.3 comes from this gene; cDNA EST yk489h9.5 com....

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23790	ENU07584	ANI61C9603: 1311..2844	32-51	807-829	LINAP		g548585	602	165	4.00E-40	47	23	poly [ADP-ribose] polymerase (PARP) (ADPRT) (NAD(+)) ADP-ribosyltransferase (poly[ADP-ribose] synthetase) ; NAD+ ADP-ribosyltransferase (EC 2.4.2.30) - fruit fly (Drosophila melanogaster) ; (D13806) poly(ADP-ribose) polymerase [Drosophila melanogaster] ; (AF051548) poly(ADP-ribose) polymerase [Drosophila melanogaster] hypothetical protein YDL201w - yeast (Saccharomyces cerevisiae) ; (X99000) ORF D1075 [Saccharomyces cerevisiae] ; (Z74249) ORF YDL201w [Saccharomyces cerevisiae] hypothetical 42.2 KD protein C17G8.11C in chromosome I ; (Z69795) unknown [Schizosaccharomyces pombe] lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] (Z98533) phosphoribosylformylglycinamide synthase [Schizosaccharomyces pombe] (AL033388) rrm3-pif1 helicase homolog [Schizosaccharomyces pombe] (AL033388) putative calcium-transporting atpase [Schizosaccharomyces pombe] (AF119122) serotonin transporter [Bos taurus]
23791	ENU07585	ANI61C6528: 2266..1157	23-43	806-825	LINAP		g2131358	535	166	1.00E-40	58	66	
23792	ENU07586	ANI61C9619: 91..512	22-45	456-479	LINAP		g1723483	97	68	4.00E-11	27	38	
23793	ENU07587	ANI61C6539: 1..1262	24-43	800-822	LINAP		g125935	574	124	3.00E-45	39	48	
23794	ENU07588	ANI61C5850: 1559..3577	22-45	727-746	LINAP		g2330857	1810	260	4.00E-69	64	20	
23795	ENU07589	ANI61C1130: 0..1245..1	22-45	726-745	LINAP		g3850110	948	185	1.00E-71	52	32	
23796	ENU07590	ANI61C9114: 1..3099	23-50	806-828	LINAP		g3850108	3130	356	8.00E-98	63	22	
23797	ENU07591	ANI61C6538: 1591..2558	22-42	796-815	LINAP		g4588918	353	75	7.00E-29	29	44	

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23798	ENU07592	ANI61C1131 4:689..1089	26-53	376-399	LINAP		g130784	126	74	8.00E-13	25	18	Pyrimidine pathway regulatory protein PPR1 - yeast 1 ; regulatory protein PPR1 - yeast (Saccharomyces cerevisiae) ; (X01739) regulatory protein (AA 1-904) [Saccharomyces cerevisiae] ; (Z73186) ORF YLR014c [Saccharomyces cerevisiae]
23799	ENU07593	ANI61C1711: 22-47 5137..3884	22-47	788-807	LINAP		g206877	980	177	4.00E-65	52	48	(M57453) sterol carrier protein-x [Rattus norvegicus]
23800	ENU07594	ANI61C9114: 22-49 4111..4459	22-49	454-479	LINAP		g2501349	89	61	0.000000	34	33	transaldolase ; (D90900) transaldolase [Synecocystis sp.]
23801	ENU07595	ANI61C5845: 22-47 4587..3480	22-47	809-828	LINAP		g1174472	181	60	0.000000	28	47	probable sucrose utilization protein SUC1
23802	ENU07596	ANI61C9134: 22-47 1..1382	22-47	796-815	LINAP		g2330690	481	146	1.00E-34	35	16	(Z98529) putative cytoskeleton assembly control protein [Schizosaccharomyces pombe]
23803	ENU07597	ANI61C1119: 26-53 9244..11350	26-53	728-748	LINAP		g119830	1655	185	2.00E-52	44	15	"fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41] ; fatty-acid synthase (EC 2.3.1.85) - Penicillium griseofulvum ; (M37461) FAS2 protein [Penicillium patulum] " (U43200) antifreeze glycopeptide AFGP polyprotein precursor [Boreogadus saida]
23804	ENU07598	ANI61C9134: 47-67 1439..2299	47-67	808-827	LINAP		g2078483	129	35	0.61	26	53	(AJ010902) invertin [Mus musculus]
23805	ENU07599	ANI61C9625: 24-47 443..1412	24-47	807-829	LINAP		g3757672	248	125	5.00E-28			hypothetical 102.7 KD protein in PRP16-SRP40 intergenic region ; hypothetical protein YKR089c - yeast (Saccharomyces cerevisiae) ; (Z27116) ORF YKR409 [Saccharomyces cerevisiae] ; (Z28314) ORF YKR089c [Saccharomyces cerevisiae]
23806	ENU07600	ANI61C1131 102-129 8:2481..1732	102-129	705-729	LINAP		g549643	284	41	0.000000			probable calcium-transporting ATPase 4 ; probable ATPase (EC 3.6.1.-) YDR093w - yeast (Saccharomyces cerevisiae) ; (Z47746) probable ATPase [Saccharomyces cerevisiae]
23807	ENU07601	ANI61C1721: 22-49 800..2490	22-49	622-649	LINAP		g2493010	1141	320	9.00E-87	55	17	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23808	ENU07602	ANI61C9117: 23-44 2011..2352	451-472	451-472	LINAP	Database Hit	g3560261	328	156	1.00E-37	48	29	(AL031535) RNA binding protein [Schizosaccharomyces pombe]
23809	ENU07603	ANI61C9635: 38-57 258..934	633-656	633-656	LINAP	Database Hit	g2842505	191	112	3.00E-24	42	46	(AL021748) adenosine deaminase [Schizosaccharomyces pombe]
23810	ENU07604	ANI61C6489: 48-67 4892..4135	709-730	709-730	LINAP	Database Hit	g2326250	140	59	0.000000	36	48	(AC004684) hypothetical protein [Arabidopsis thaliana]
23811	ENU07605	ANI61C5883: 23-42 3020..2339	639-661	639-661	LINAP	Database Hit	g1168610	379	99	2.00E-41	41		"Asparagine-rich zinc finger protein AZF1; finger protein AZF1, asparagine-rich - yeast (Saccharomyces cerevisiae); (Z26253) zinc finger protein of 101170 Da [Saccharomyces cerevisiae]; (X90518) ORF O3244 [Saccharomyces cerevisiae]; (X94335) YOR3244w [Saccharomyces cerevisiae]; (Z75021) ORF YOR113w [Saccharomyces cerevisiae]"
23812	ENU07606	ANI61C1718: 22-49 4412..3576	792-815	792-815	LINAP	Database Hit	g171106	195	101	9.00E-21	26	83	(M61773) ATP12 [Saccharomyces cerevisiae]
23813	ENU07607	ANI61C6547: 22-46 493..988	452-479	452-479	LINAP	Database Hit	g1208874	87	70	9.00E-12	30	8	(U50071) C. elegans ankyrin-related unc-44 (GB:U21734) [Caenorhabditis elegans]; (U39847) AO66 ankyrin [Caenorhabditis elegans]
23814	ENU07608	ANI61C1132 6:1590..2375			LINAP	Database Hit	g3417437	227	65	5.00E-10	36	73	(AL031263) putative GTPase-activator protein for Rho-like GTPases [Schizosaccharomyces pombe]
23815	ENU07609	ANI61C1735: 22-43 1650..417	699-721	699-721	LINAP	Database Hit	g1705871	1276	335	e-104	88	48	"citrate synthase, mitochondrial precursor; (D63376) citrate synthase precursor [Aspergillus niger]"
23816	ENU07610	ANI61C1745: 34-59 3133..2756	446-465	446-465	LINAP	Database Hit	g4567277	104	49	0.00002	34	11	(AC006841) putative pol protein with Zn finger CCHC type domain [Arabidopsis thaliana]
23817	ENU07611	ANI61C5888: 156-183 4057..3501	448-467	448-467	LINAP	Database Hit	g1083757	323	112	1.00E-31	43	15	plasma membrane Ca2+-ATPase isoform 4 - rat; (U15408) plasma membrane Ca2+-ATPase isoform 4 [Rattus norvegicus]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23830	ENU07624	ANI61C9601: 35-55 930..1297	55-55	452-479	LINAP		g1351343	103	36	0.23	30	11	positive regulator of purine utilisation ; positive regulator of purine utilisation - Emmericella nidulans ; (X84015)
23831	ENU07625	ANI61C6553: 24-43 3275..2800	24-43	452-479	LINAP		g1673402	145	65	3.00E-10			positive regulator of purine utilisation [Emmericella nidulans] (Z82044) hypothetical 54.4 kd protein [Bacillus subtilis]
23832	ENU07626	ANI61C1734: 47-74 5554..4663	47-74	806-828	LINAP		g3327206	300	150	9.00E-36	39	41	(AB014596) KIAA0696 protein [Homo sapiens]
23833	ENU07627	ANI61C2767: 27-46 651..1125	27-46	375-394	LINAP		g1168457	101	85	2.00E-16	35	8	ANKYRIN ; ankyrin - mouse ; (M84756) ankyrin [Mus musculus] (U46069) fertilin alpha subunit [Oryctolagus cuniculus]
23834	ENU07628	ANI61C9145: 22-49 2397..1682	22-49	671-695	LINAP		g1245061	78	55	0.000000			Pyrimidine pathway regulatory protein 1 ; regulatory protein PPR1 - yeast (Saccharomyces cerevisiae) ; (X01739) regulatory protein (AA 1-904) [Saccharomyces cerevisiae] ; (Z73186) ORF YLR014c [Saccharomyces cerevisiae]
23835	ENU07629	ANI61C9601: 55-74 1822..2247	55-74	422-442	LINAP		g130784	79	74	8.00E-13	31	18	
23836	ENU07630	ANI61C1131: 22-45 2884..1508	22-45	805-827	LINAP		g3261605	579	146	6.00E-43	41	13	(Z74697) ppsA [Mycobacterium tuberculosis]
23837	ENU07631	ANI61C1757: 22-45 1867..2501	22-45	568-590	LINAP		g3184102	185	127	7.00E-29	37	32	(AL023777) hypothetical protein [Schizosaccharomyces pombe]
23838	ENU07632	ANI61C2764: 65-91 1339..358	65-91	803-829	LINAP		g1147800	1005	254	e-101	78	57	(U43720) Sug2p [Saccharomyces cerevisiae]
23839	ENU07633	ANI61C9144: 22-46 2094..2560	22-46	458-479	LINAP		g2388584	69	38	0.046			(AC000098) EST gb ATTS1136 comes from this gene. [Arabidopsis thaliana] hypothetical 44.9 KD protein C18B11.02C in chromosome I ; hypothetical protein SPAC18B11.02c - fission yeast (Schizosaccharomyces pombe) ; (Z50728) hypothetical protein [Schizosaccharomyces pombe]
23840	ENU07634	ANI61C6543: 22-49 659..1663	22-49	808-827	LINAP		g1175381	773	251	5.00E-66	50	63	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23841	ENU07635	ANI61C5903: 496..1	121-142	461-479	LINAP		g115875	155	85	2.00E-16	33	48	CBP3 protein precursor ; membrane protein CBP3 - yeast (Saccharomyces cerevisiae) ; (J04830) CBP3 protein [Saccharomyces cerevisiae] ; (Z73571) ORF YPL215w [Saccharomyces cerevisiae] (X97001) LR8B [Gallus gallus]
23842	ENU07636	ANI61C1747: 31-50	430-450		LINAP		g1595750	34	59	0.000000			Pectate lyase L precursor ; (L42248)
23843	ENU07637	ANI61C2775: 22-48	682-705		LINAP		g3914287	134	69	2.00E-16	30	50	pectate lyase [Erwinia chrysanthemi] "(AC002292) similar to "Mx" GTP-binding proteins [Arabidopsis thaliana]
23844	ENU07638	ANI61C9628: 23-46	493-512		LINAP		g2462747	44	49	0.00002	32	17	"
23845	ENU07639	ANI61C5931: 29-48	438-457		LINAP		g1723807	161	54	0.000000	21	25	hypothetical 70.6 KD protein in PGDI-STT3 intergenic region ; hypothetical protein YGL023c - yeast (Saccharomyces cerevisiae) ; (Z72545) ORF YGL023c [Saccharomyces cerevisiae]
23846	ENU07640	ANI61C1135 7:407..1430	28-48	805-829	LINAP		g2894292	68	63	0.000000			"(AL021837) SPBC947.05c, ferric reductase transmembrane component, (possibility of intron between 15640-15725 but FASTA suggests not), len:564aa, similar eg. to S. pombe, FRP1_SCHPO, Q04800, ferric reductase transmembrane compon..."
23847	ENU07641	ANI61C1747: 3506..2751	109-128	710-735	LINAP		g2648250	178	97	1.00E-19	31	33	(AE000948) 3-hydroxyacyl-CoA dehydrogenase (hbd-10) [Archaeoglobus fulgidus]
23848	ENU07642	ANI61C9161: 1266..1	22-48	722-744	LINAP		g3650382	579	190	8.00E-48	38	28	(AL031740) putative calcium dependant serine-threonine protein kinase. [Schizosaccharomyces pombe]
23849	ENU07643	ANI61C9628: 3696..4135	43-61	459-478	LINAP		g131767	63	53	0.000001			Quinic acid utilization activator ; regulatory protein QUTA - Emericella nidulans ; (X06252) QUTA protein (AA 1 - 825) [Emericella nidulans] (AL023533) hypothetical protein [Schizosaccharomyces pombe]
23850	ENU07644	ANI61C2801: 1..321	115-132	270-289	LINAP		g3130058	167	47	2.00E-11	51	11	

Genomic Context

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23851	ENU07645	ANI61C6552: 22-44 5929..4882	803-822	803-822	LINAP		g1208874	430	167	8.00E-41	34	15	(U50071) C. elegans ankyrin-related unc-44 (GB:U21734) [Caenorhabditis elegans] ; (U39847) AO66 ankyrin [Caenorhabditis elegans]
23852	ENU07646	ANI61C1137 22-48 9:4059..4439	375-397	375-397	LINAP		g3023956	87	75	3.00E-13			vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospora anserina]
23853	ENU07647	ANI61C1765: 75-94 864..1	729-749	729-749	LINAP		g2499128	220	79	4.00E-18	34	38	vacuolar protein sorting-associated protein VPS5 ; (U73512) Vps5p [Saccharomyces cerevisiae] ; (U84735) Vps5p [Saccharomyces cerevisiae]
23854	ENU07648	ANI61C2801: 79-98 959..1393	356-380	356-380	LINAP		g2497170	97	44	0.0008			hypothetical 85.0 KD protein in HLJ1-SMP2 intergenic region ; hypothetical protein YMR164c - yeast (Saccharomyces cerevisiae) ; (Z49705) unknown [Saccharomyces cerevisiae] TRNA splicing protein SPL1 ; (AF000115) tRNA splicing protein [Candida maltosa]
23855	ENU07649	ANI61C6608: 75-94 254..836	359-381	359-381	LINAP		g2492879	698	290	6.00E-78	72	39	(Z99104) similar to cell-cycle protein [Bacillus subtilis]
23856	ENU07650	ANI61C1139 32-59 5:204..1067	803-829	803-829	LINAP		g2632334	75	61	0.000000			(X71807) uric acid-xanthine permease [Emericella nidulans]
23857	ENU07651	ANI61C1807: 480..1820			LINAP		g3286685	1908	392	e-121	92	39	(AJ012627) haloalkane dehalogenase [Mycobacterium sp.]
23858	ENU07652	ANI61C9140: 22-49 1710..2011	449-468	449-468	LINAP		g3860531	94	41	0.000000	28	37	(AL021839) putative nuclear pore protein [Schizosaccharomyces pombe]
23859	ENU07653	ANI61C1806: 23-42 1773..2999	721-740	721-740	LINAP		g2894271	326	112	3.00E-24	30	69	(AC000133) ORF [Emericella nidulans]
23860	ENU07654	ANI61C9147: 49-68 3471..4684	805-824	805-824	LINAP		g1870209	245	111	5.00E-24	28	50	(AL035065) putative urea active transporter [Schizosaccharomyces pombe]
23861	ENU07655	ANI61C59:11 22-41 36..361	537-556	537-556	LINAP		g4106690	339	109	2.00E-28	48	30	hypothetical 59.1 KD protein ZK637.1 in chromosome III
23862	ENU07656	ANI61C1140 24-47 3:689..292	448-467	448-467	LINAP		g586797	57	70	1.00E-11			"(X80835) len: 676, CAL: 0.13 [Saccharomyces cerevisiae] "
23863	ENU07657	ANI61C7181: 25-52 1094..1718	584-603	584-603	LINAP		g530340	141	65	4.00E-10	25	30	(AL049498) rho1 gdp-gtp exchange protein 1 [Schizosaccharomyces pombe]
23864	ENU07658	ANI61C7196: 1384..1			LINAP		g4539279	1069	346	2.00E-94	64	20	

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23865	ENU07659	ANI61C2840: 32-58 2281..1	713-732	713-732	LINAP		g2500542	1356	79	1.00E-18			putative ATP-dependent RNA helicase YMR128W; probable membrane protein YMR128w - yeast (Saccharomyces cerevisiae); (Z48622) unknown [Saccharomyces cerevisiae] (AJ011965) oxidoreductase [Claviceps purpurea] choline-phosphate cytidyltransferase (EC 2.7.7.15) - yeast (Saccharomyces cerevisiae); (Z49133) cholinephosphate cytidyltransferase [Saccharomyces cerevisiae]; (Z72987) ORF YGR202c [Saccharomyces cerevisiae]
23866	ENU07660	ANI61C9655: 56-76 1827..1442	314-333	314-333	LINAP		g4499843	124	52	0.000001			
23867	ENU07661	ANI61C6602: 22-49 829..1979	808-829	808-829	LINAP		g2144437	640	178	2.00E-69	55	57	
23868	ENU07662	ANI61C2875: 28-50 978..595	266-289	266-289	LINAP		g728783	204	126	1.00E-28	41	21	putative aconitase in PRP21-UBP12 intergenic region; aconitate hydratase homolog YJL200c - yeast (Saccharomyces cerevisiae); (X77688) hypothetical protein J0327 [Saccharomyces cerevisiae]; (Z49475) ORF YJL200c [Saccharomyces cerevisiae]
23869	ENU07663	ANI61C9645: 45-64 2268..3125	785-803	785-803	LINAP		g4008556	296	111	2.00E-32	40	69	(AL034490) putative lectin precursor [Schizosaccharomyces pombe]
23870	ENU07664	ANI61C183:1 137..1	729-749	729-749	LINAP		g3182891	1746	513	e-145	98	70	Actin; (AJ000335) actin [Botryotinia fuckeliana]
23871	ENU07665	ANI61C2835: 23-50 1..2645	798-817	798-817	LINAP		g3510629	525	123	1.00E-27	32	2	(AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae]
23872	ENU07666	ANI61C9163: 22-49 616..1967	805-829	805-829	LINAP		g4099313	386	161	3.00E-40	42	2	(U85909) peptide synthetase [Aureobasidium pullulans]
23873	ENU07667	ANI61C6535: 22-44 9996..9601	429-448	429-448	LINAP		g630885	124	71	4.00E-12	32	39	"Sp1/egr-like zinc-finger protein - fruit fly (Drosophila sp.); (S71230) Sp1/egr-like zinc-finger protein=hkb [Drosophila, 0-4 hr embryos, Peptide, 296 aa] [Drosophila sp.]; huckebein gene [Drosophila melanogaster]"
23874	ENU07668	ANI61C1758: 23-50 1213..565	609-628	609-628	LINAP		g2459421	312	94	6.00E-29	47	74	(AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]

Sequence Annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23875	ENU07669	ANI61C9146: 1..595	222-241	363-380	LINAP		g128831	641	200	5.00E-67			"mitochondrial nuclease ; nuclease NUC1 (EC 3.1.30.-) precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X06670) nuclease [Saccharomyces cerevisiae] ; (Z34098) ORF [Saccharomyces cerevisiae] ; (X77688) mitochondrial nuclease [Saccharomyces cerevisiae] ; (Z49483) ORF YJL208c [Saccharomyces cerevisiae] "
23876	ENU07670	ANI61C9678: 1001..1846	22-45	795-815	LINAP		g730615	139	118	6.00E-26			DNA-directed RNA polymerase mitochondrial precursor ; (L25087) mitochondrial RNA polymerase [Neurospora crassa] ; cyt-5 gene [Neurospora crassa]
23877	ENU07671	ANI61C6535: 9039..8508	110-137	491-510	LINAP		g1345773	116	35	0.33			Chromodomain-helicase-DNA-binding protein 1 (CHD-1) ; (L10410) DNA-binding protein [Mus musculus]
23878	ENU07672	ANI61C59:45 22-45 75..5192	22-45	561-580	LINAP		g2851420	181	103	9.00E-22	27	26	"hypothetical 88.1 KD protein in GLTS-SELC intergenic region ; (AE000443) orf, hypothetical protein [Escherichia coli] "
23879	ENU07673	ANI61C7187: 36-53 3306..2556	36-53	622-641	LINAP		g586312	107	55	6.00E-14	24	37	hypothetical 63.4 KD protein in SMY2-RPS101 intergenic region ; probable resistance protein - yeast (Saccharomyces cerevisiae) ; (Z36049) ORF YBR180w [Saccharomyces cerevisiae]
23880	ENU07674	ANI61C6605: 485..850	22-49	422-441	LINAP		g2132942	67	65	4.00E-10			probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae) ; (Z75214) ORF YOR306c [Saccharomyces cerevisiae]
23881	ENU07675	ANI61C5928: 26-53 3691..2752	26-53	744-767	LINAP		g2414637	988	332	2.00E-90	58	37	(Z99260) probable na(+)-h(+) antiporter [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23882	ENU07676	ANI61C1139 7:4176..2829	23-42	808-829	LINAP		g729417	403	142	3.00E-41	38	42	GAA1 protein ; membrane protein END2 - yeast (Saccharomyces cerevisiae) ; (X79409) Gaa1 [Saccharomyces cerevisiae] ; (U53880) Gaa1p [Saccharomyces cerevisiae] ; (Z73260) ORF YLR088w [Saccharomyces cerevisiae] (AJ223999) PCZA363.5 [Amycolatopsis orientalis] (M77661) putative pol polyprotein [Magnaporthe grisea] hypothetical 50.6 KD protein in RPL14B-GPA1 intergenic region ; hypothetical protein YHR004c - yeast (Saccharomyces cerevisiae) ; (U10555) Yhr004cp [Saccharomyces cerevisiae] (AL049521) hypothetical protein [Schizosaccharomyces pombe] (AB015510) Fli-CMCase [Aspergillus aculeatus] hypothetical 65.3 KD protein in PRE3- SAG1 intergenic region ; hypothetical protein YJR001w - yeast (Saccharomyces cerevisiae) ; (X87611) ORF YJR83.4 [Saccharomyces cerevisiae] ; (Z49501) ORF YJR001w [Saccharomyces cerevisiae] (AL023592) rna binding protein [Schizosaccharomyces pombe] "N2,N2-dimethylguanosine TRNA methyltransferase precursor ; N2,N2- dimethylguanine tRNA methyltransferase - yeast (Saccharomyces cerevisiae) ; (M17193) tRNA dimethyltransferase [Saccharomyces cerevisiae] ; (Z48758) Trm1p [Saccharomyces cerevisiae] "
23883	ENU07677	ANI61C6605: 1777..2165	22-49	451-470	LINAP		g2894190	71	58	0.000000 04	30	6	
23884	ENU07678	ANI61C1136: 2200..906	63-90	733-760	LINAP		g538067	463	176	2.00E-43	39	20	
23885	ENU07679	ANI61C2838: 4406..5240	28-47	781-808	LINAP		g731630	339	94	5.00E-34	41	53	
23886	ENU07680	ANI61C9153: 3411..2201	35-54	771-790	LINAP		g4539592	458	115	1.00E-41	35	46	
23887	ENU07681	ANI61C6623: 430..1	117-137	453-479	LINAP		g3242653	262	87	2.00E-23	57	27	
23888	ENU07682	ANI61C5970: 378..1	107-127	454-478	LINAP		g1353046	302	134	4.00E-31	39	27	
23889	ENU07683	ANI61C1139 9:3306..4594	22-41	723-749	LINAP		g3136059	194	98	1.00E-19	27	19	
23890	ENU07684	ANI61C7223: 1606..1	29-50	611-630	LINAP		g136242	781	146	1.00E-34	42	42	

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23891	ENU07685	ANI61C6601: 3930..3485	22-45	445-465	LINAP		g1176495	94	111	4.00E-24	36	22	hypothetical 79.4 KD protein in PRP16-SRP40 intergenic region ; (Z28315) ORF YKR090w [Saccharomyces cerevisiae]
23892	ENU07686	ANI61C9170: 22-42 3667..4819	22-42	772-799	LINAP		g3876393	843	138	5.00E-47	53	68	(Z79695) Similarity to Human 2-oxoisovalerate dehydrogenase (SW:ODBB_HUMAN) [Caenorhabditis elegans]
23893	ENU07687	ANI61C9674: 22-47 807..441	22-47	452-471	LINAP		g3912958	128	44	0.000003	47	24	alpha-L-arabinofuranosidase precursor (arabinosidase) ; (AL021411) arabinofuranosidase [Streptomyces coelicolor]
23894	ENU07688	ANI61C1139: 34-53 1905..1591	34-53	452-479	LINAP		g1934826	71	50	0.000008	30	47	(Z93938) unknown [Bacillus subtilis]
23895	ENU07689	ANI61C9184: 30-57 2382..2699	30-57	457-479	LINAP		g3947870	52	36	0.23			(AL034382) hypothetical protein [Schizosaccharomyces pombe]
23896	ENU07690	ANI61C6633: 39-58 627..969	39-58	448-475	LINAP		g3646455	436	88	3.00E-17	73	43	(AL031603) 60s ribosomal protein [Schizosaccharomyces pombe]
23897	ENU07691	ANI61C5982: 56-75 1258..541	56-75	665-684	LINAP		g1730644	271	120	1.00E-26	32	36	hypothetical 73.4 KD protein in ERG24-MET2 intergenic region ; probable membrane protein YNL279w - yeast (Saccharomyces cerevisiae) ; (Z71555) ORF YNL279w [Saccharomyces cerevisiae]
23898	ENU07692	ANI61C1139: 68-87 2758..2293	68-87	430-449	LINAP		g3915558	122	73	1.00E-12	33	44	hypothetical 36.5 KD protein in GBSA-TLPB intergenic region ; (Z99119) similar to hypothetical proteins [Bacillus subtilis]
23899	ENU07693	ANI61C1869: 26-45 662..1	26-45	519-546	LINAP		g2492777	413	113	5.00E-35	47	59	hypothetical zinc-type alcohol dehydrogenase-like protein in PRE5-FET4 intergenic region ; hypothetical protein YMR318c - yeast (Saccharomyces cerevisiae) ; (Z54141) unknown [Saccharomyces cerevisiae]
23900	ENU07694	ANI61C5985: 44-64 512..1	44-64	453-480	LINAP		g3885836	196	67	8.00E-11	41	24	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
23901	ENU07695	ANI61C1907: 52-71 534..1	52-71	456-475	LINAP		g2315274	159	88	4.00E-17	40	46	(Y11113) endoglucanase IV [Hypocrea jecorina]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23902	ENU07696	ANI61C9180: 23-50 1991..1668	23-50	452-479	LINAP			55			24		
23903	ENU07697	ANI61C5987: 32-51 576..1052	32-51	457-479	LINAP		g3925783	263	130	6.00E-30	49	32	(AL034353) glutamate n-acetyltransferase precursor [Schizosaccharomyces pombe]
23904	ENU07698	ANI61C1143: 22-46 0:2733..3362	22-46	578-603	LINAP		g4501925	252	75	6.00E-13	40	41	adducin 1 (alpha) ; (Z68280) Human tetracycline transporter-like protein mRNA [Homo sapiens]
23905	ENU07699	ANI61C1142: 26-45 7:997..1438	26-45	458-477	LINAP		g4502601	168	82	3.00E-15	32	53	carboxyl reductase 3 ; (AB004854) carboxyl reductase 3 [Homo sapiens] ; (AB003151) carbonyl reductase 3 [Homo sapiens]
23906	ENU07700	ANI61C9663: 5432..5009			LINAP		g2133058	178	87	6.00E-17	33	41	probable transcription factor YPL230w - yeast (Saccharomyces cerevisiae) ; (X94561) transcription factor [Saccharomyces cerevisiae] ; (Z73586) ORF YPL230w [Saccharomyces cerevisiae]
23907	ENU07701	ANI61C2977: 106-124 359..1	106-124	454-479	LINAP		g476334	220	71	1.00E-21	44	33	(U07801) serine/threonine/tyrosine kinase [Ustilago maydis]
23908	ENU07702	ANI61C7261: 1363..1008			LINAP		g2853097	130	69	2.00E-11	48	56	(AL021767) hypothetical protein [Schizosaccharomyces pombe]
23909	ENU07703	ANI61C6642: 25-52 106..607	25-52	454-481	LINAP		g2984067	51	60	0.000000	35	18	(AE000755) transketolase [Aquifex aeolicus]
23910	ENU07704	ANI61C2968: 54-74 1245..741	54-74	420-439	LINAP		g1350795	254	126	1.00E-28	40	64	"mitochondrial 60S ribosomal protein L24 precursor (YML24) ; ribosomal protein YmL24, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z47815) ribosomal protein [Saccharomyces cerevisiae] "
23911	ENU07705	ANI61C6595: 22-46 1021..1	22-46	722-741	LINAP		g450864	939	286	3.00E-88	61	47	(L27993) alkaline phosphatase [Neurospora crassa]
23912	ENU07706	ANI61C5991: 26-48 1321..625	26-48	644-663	LINAP		g1654028	178	61	0.000000	27	50	(Z81360) hypothetical protein Rv1726 [Mycobacterium tuberculosis]
23913	ENU07707	ANI61C1894: 38-57 2439..4124	38-57	731-750	LINAP		g2851420	1248	178	6.00E-79	56	33	"hypothetical 88.1 KD protein in GLTS-SELC intergenic region ; (AE000443) orf, hypothetical protein [Escherichia coli] "

Gene ID "0654166"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23914	ENU07708	ANI61C9673: 24-43 5828..5111	481-502	481-502	LINAP		g1806234	134	68	4.00E-17	31	78	(Z84498) hypothetical protein Rv1928c [Mycobacterium tuberculosis]
23915	ENU07709	ANI61C5961: 22-45 2804..2047	705-732	705-732	LINAP		g4501975	80	43	0.002			beta3A-adaptin ; (U91931) AP-3 complex beta3A subunit [Homo sapiens]
23916	ENU07710	ANI61C1036 22-49 3:1246..1693	453-479	453-479	LINAP		g3417427	94	45	0.0005			(AL031262) hypothetical protein [Schizosaccharomyces pombe]
23917	ENU07711	ANI61C2978: 63-90 668..1	557-582	557-582	LINAP		g1706559	118	54	0.000000 31 003	31	32	Ethanolamine kinase (easily shocked protein) ; (L35603) ethanolamine kinase [Drosophila melanogaster]
23918	ENU07712	ANI61C9701: 27-47 3206..3928	585-604	585-604	LINAP		g3850091	319	128	2.00E-37	43	42	(AL033389) putative aminotransferase [Schizosaccharomyces pombe]
23919	ENU07713	ANI61C6593: 2302..1			LINAP		g586510	1022	118	1.00E-35	45	28	hypothetical 108.0 KD helicase in HSP26-TIF32 intergenic region ; probable DNA repair protein - yeast (Saccharomyces cerevisiae) ; (X76294) ORF YBRO715; homologous to Rad54 Snf2 and Sth1 of S.cerevisiae [Saccharomyces cerevisiae] ; (Z35942) ORF YBR073w [Saccharomyces cerevisiae]
23920	ENU07714	ANI61C599:2 23-48 247..1	719-737	719-737	LINAP		g1174555	1182	170	5.00E-49	43	28	putative transcription initiation factor TFIID 111 KD subunit (TBP-associated factor 111 KD) (TAFII-111) ; hypothetical protein SPAC2G11.14 - fission yeast (Schizosaccharomyces pombe) ; (Z54354) putative transcription initiation factor tfiid subunit [Schizosaccharomyces pombe]
23921	ENU07715	ANI61C1044 38-57 3:2002..2587	531-551	531-551	LINAP		g624076	80	45	0.0004			"(U42580) contains Pro-rich Px motifs: SPKPP (20X), PEPPA (9X); similar to soybean pro-rich cell wall protein, corresponds to Swiss-Prot Accession Number P13993 [Paramecium bursaria Chlorella virus 1]"
23922	ENU07716	ANI61C9675: 24-43 5744..6242	454-478	454-478	LINAP		g1085697	123	80	1.00E-14	29	36	chitin deacetylase - Mucor rouxii (fragment)
23923	ENU07717	ANI61C5953: 24-43 993..555	453-479	453-479	LINAP		g4456816	371	126	9.00E-29	34	17	(AL035548) hypothetical protein [Schizosaccharomyces pombe]

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23924	ENU07718	ANI61C2959: 22-48 1..1071	778-798	778-798	LINAP		g3877858	130	41	0.008	21	24	Similarity with drosophila (Z34801) Similarity with drosophila MSP-300 protein (PIR acc. no. S30431) [Caenorhabditis elegans] ; (Z66514) Similarity with drosophila MSP-300 protein (PIR acc. no. S30431) [Caenorhabditis elegans] (X93302) Msn5 protein [Saccharomyces cerevisiae] (AF111068) DNA polymerase gamma [Neurospora crassa] "alcohol dehydrogenase (ADH-T) ; alcohol dehydrogenase (EC 1.1.1.1), thermostable - Bacillus stearothermophilus ; (D90421) alcohol dehydrogenase [Bacillus stearothermophilus] " (AB001895) B120 [Homo sapiens] (AL023534) hypothetical protein [Schizosaccharomyces pombe] (AF051140) putative glucose transporter protein [Schizosaccharomyces pombe] "(AE001002) ATP-dependent RNA helicase, putative [Archaeoglobus fulgidus] " hypothetical 93.9 KD helicase C19G10.02 in chromosome I ; (Z69909) dna repair protein [Schizosaccharomyces pombe] (AL022600) hypothetical protein [Schizosaccharomyces pombe] hypothetical 187.1 KD protein in OGG1-CNA2 intergenic region ; probable membrane protein YML059c - yeast (Saccharomyces cerevisiae) ; (Z46729) unknown [Saccharomyces cerevisiae]
23925	ENU07719	ANI61C9693: 29-56 3518..378	805-829	805-829	LINAP		g1246837	411	61	0.000000			
23926	ENU07720	ANI61C7224: 22-49 3886..663	802-829	802-829	LINAP		g4455007	3371	377	e-104	67	21	
23927	ENU07721	ANI61C6624: 41..971			LINAP		g1168347	270	53	9.00E-17	34	65	
23928	ENU07722	ANI61C1059 24-43 0..2443..1234	804-823	804-823	LINAP		g2588991	148	38	0.12			
23929	ENU07723	ANI61C3017: 102-120 1011..410	471-490	471-490	LINAP		g3130035	348	129	2.00E-32	40	29	
23930	ENU07724	ANI61C9716: 22-44 947..1	773-796	773-796	LINAP		g3746450	135	59	0.000000	27	36	
23931	ENU07725	ANI61C6617: 40-59 1820..3569	791-810	791-810	LINAP		g2649107	798	119	3.00E-31	33	35	
23932	ENU07726	ANI61C6009: 87-106 1244..451	666-685	666-685	LINAP		g1723497	371	187	6.00E-47	47	27	
23933	ENU07727	ANI61C6621: 39-62 4620..3659	761-780	761-780	LINAP		g3080533	258	145	5.00E-34	42	33	
23934	ENU07728	ANI61C600:1 26-53 273..1	723-742	723-742	LINAP		g2501686	596	207	9.00E-53	42	16	

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23935	ENU07729	ANI61C6011: 610..1027	34-53	413-432	LINAP		g2120949	94	64	5.00E-10	36	22	lipase-like enzyme - Alcaligenes eutrophus ; (L36817) lipase-like enzyme [Alcaligenes eutrophus] ; ORF 8 [Ralstonia eutropha]
23936	ENU07730	ANI61C6030: 22-47	427-454		LINAP		g4098421	132	71	7.00E-12	35	19	(U77581) sugar transporter 3 [Pichia stipitis]
23937	ENU07731	ANI61C3004: 22-49	737-764		LINAP		g1169440	5402	321	e-135	96	6	"Dynein heavy chain, cytosolic (DYHC) ; cytoplasmic dynein heavy chain - Emericella nidulans ; (U03904) cytoplasmic dynein [Emericella nidulans]"
23938	ENU07732	ANI61C972:1 37-58	409-433		LINAP		g2842510	204	106	1.00E-22	45	15	(AL021748) hypothetical protein [Schizosaccharomyces pombe]
23939	ENU07733	ANI61C9702: 68-87	735-759		LINAP		g2497203	164	48	3.00E-13	26	15	hypothetical 180.2 KD protein in FAA4-HOR7 intergenic region ; probable membrane protein YMR247c - yeast (Saccharomyces cerevisiae)
23940	ENU07734	ANI61C6675: 918..1244			LINAP		g1723187	107	39	0.00005			"112.3 KD protein in PYK1-SNC1 intergenic region ; FUN12 protein - yeast (Saccharomyces cerevisiae) ; (U12980) Fun12p: 97kDa protein, function unknown [Saccharomyces cerevisiae]"
23941	ENU07735	ANI61C1136 122-145	442-467		LINAP		g1764098	51	41	0.004			(U81794) putative permease [Uromyces fabae]
23942	ENU07736	ANI61C9235: 32-52	403-425		LINAP		g3929366	714	155	1.00E-50	77	73	40S ribosomal protein S7 ; (U73847) ribosomal protein [Neurospora crassa]
23943	ENU07737	ANI61C7286: 33-52	655-673		LINAP		g625653	575	136	3.00E-51	54	27	ATP-dependent proteinase BsgA - Myxococcus xanthus
23944	ENU07738	ANI61C9700: 22-48	439-466		LINAP		g121649	150	51	8.00E-17	31	17	GRR1 protein ; GRR1 protein - yeast (Saccharomyces cerevisiae) ; (M59247) putative [Saccharomyces cerevisiae] ; (Z49590) ORF YJR090c [Saccharomyces cerevisiae] ; (L47993) ORF YJR090c [Saccharomyces cerevisiae]
23945	ENU07739	ANI61C1500: 22-45	366-385		LINAP		g2257705	141	71	3.00E-12	31	11	(D63905) ubiquitin ligase [Saccharomyces cerevisiae]

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23946	ENU07740	ANI61C7292: 1197..496	22-49	639-658	LINAP		g2887409	90	60	0.000000 02	30	27	(AB007877) KIAA0417 [Homo sapiens]
23947	ENU07741	ANI61C6688: 907..1343	116-135	381-399	LINAP		g4582195	195	100	8.00E-21	34	17	(Z99532) hypothetical protein [Schizosaccharomyces pombe]
23948	ENU07742	ANI61C1432: 3416..3809	47-73	262-289	LINAP		g1166378	80	44	0.0008	26	14	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
23949	ENU07743	ANI61C9221: 592..1377	22-40	745-765	LINAP		g1711542	80	48	0.00007	23	76	SSO2 protein; syntaxin-related protein SSO2 - yeast (Saccharomyces cerevisiae); (Z49808) unknown [Saccharomyces cerevisiae]
23950	ENU07744	ANI61C9697: 4700..4381	62-81	414-433	LINAP		g4100623	97	62	0.000000 003	32	27	(AF001630) SH3P18-like WASP associated protein [Homo sapiens]
23951	ENU07745	ANI61C7292: 1644..1233	22-43	457-476	LINAP		g115573	46	41	0.004			CAMP binding protein CABP1A/CABP1B (CABP1 protein); CABP1 protein - slime mold (Dictyostelium discoideum); (X52688) CABP1 protein [Dictyostelium discoideum]; (M36176) cAMP binding protein [Dictyostelium discoideum] (AL033497) unknown hypothetical protein [Candida albicans]
23952	ENU07746	ANI61C6692: 1..345	102-126	293-312	LINAP		g3859703	104	48	0.00002	34	12	ryanodine receptor [Oryctolagus cuniculus]
23953	ENU07747	ANI61C1726: 903..1554	40-59	594-613	LINAP		g226386	88	45	0.0004	28	2	(Z99714) bK1048E9.2 (similar to CE02118) [Homo sapiens]
23954	ENU07748	ANI61C6692: 954..1488	44-68	413-434	LINAP		g4455408	137	78	6.00E-14	22	31	6-hydroxy-D-nicotine oxidase (6-HDNO); (X05999) 6-hydroxy-D-nicotine oxidase [Arthrobacter oxidans]
23955	ENU07749	ANI61C3030: 1689..1370	39-58	277-299	LINAP		g122805	170	62	0.000000 002	39	23	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium; (D83643) polyketide synthase [Colletotrichum lagenarium] (U53876) Cdc45p: assembles into a complex with Cdc46p/Mcm5p [Saccharomyces cerevisiae]
23956	ENU07750	ANI61C923: 457..2487	50-69	809-829	LINAP		g2147662	86	64	0.000000 001	21	10	transcription factor nft1 - fission yeast (Schizosaccharomyces pombe)
23957	ENU07751	ANI61C9750: 1120..549	70-92	520-539	LINAP		g1256852	202	34	0.85			
23958	ENU07752	ANI61C7276: 717..341	22-42	457-477	LINAP		g626072	69	54	0.000000 7	26	16	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23968	ENU07762	ANI61C3806: 22-49 1576..2142	22-49	528-546	LINAP		g586486	114	65	4.00E-10	23	24	hypothetical 77.3 KD protein in FIG1- GIP1 intergenic region ; probable membrane protein YBR043c - yeast (Saccharomyces cerevisiae) ; (Z35912) ORF YBR043c [Saccharomyces cerevisiae]
23969	ENU07763	ANI61C6661: 22-49 1080..1751	22-49	627-649	LINAP		g2257523	319	159	2.00E-38	43	57	(AB004537) lipote-protein ligase A [Schizosaccharomyces pombe]
23970	ENU07764	ANI61C297:9 744..10255			LINAP		g4160573	125	60	4.00E-11	34	16	(AL035226) guanine nucleotide binding protein beta subunit-like [Schizosaccharomyces pombe]
23971	ENU07765	ANI61C3818: 22-41 2391..1914	22-41	440-459	LINAP		g3006139	352	100	2.00E-37	54	37	(AL022299) hypothetical protein [Schizosaccharomyces pombe]
23972	ENU07766	ANI61C9698: 22-43 8097..8486	22-43	427-451	LINAP		g1708501	84	49	0.000000	34	7	Integrin alpha chain-like protein (alpha- INT1) ; (U35070) integrin-like protein alpha Int1p [Candida albicans]
23973	ENU07767	ANI61C7307: 67-94 523..1333	67-94	768-790	LINAP		g136125	166	94	9.00E-19	30	30	putative AC transposase (ORFA) ; (X05424) ORFa [Zea mays]
23974	ENU07768	ANI61C6716: 111-130 2520..2076	111-130	341-360	LINAP		g731872	66	65	2.00E-10			"putative 108.8 KD transcriptional regulatory protein in FKH1-STH1 intergenic region ; probable membrane protein YIL130w - yeast (Saccharomyces cerevisiae) ; (Z38059) orf, len: 964, CAl: 0.15, possible regulatory protein [Saccharomyces cerevisiae]"
23975	ENU07769	ANI61C1918: 22-40 2568..660	22-40	796-815	LINAP		g113449	1374	168	4.00E-41	55	25	"probable ATP-dependent permease precursor ; ATP-dependent permease ADP1 precursor - yeast (Saccharomyces cerevisiae) ; (X59720) YCR011c, len:1049 [Saccharomyces cerevisiae]"
23976	ENU07770	ANI61C3066: 22-44 879..134	22-44	660-679	LINAP		g2246452	106	50	0.00002	31	34	(U71107) S-adenosyl-methionine- sterol-C-methyltransferase homolog [Nicotiana tabacum]
23977	ENU07771	ANI61C9727: 33-53 642..1451	33-53	758-779	LINAP		g2656003	734	271	4.00E-72	69	74	(Z98980) hypothetical protein [Schizosaccharomyces pombe]

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23978	ENU07772	ANI61C6686: 22-49 981..219	563-584	LINAP			g731298	219	59	5.00E-16	36	35	probable transporter SEO1 ; probable membrane protein YAL067c - yeast (Saccharomyces cerevisiae) ; (U12980) Seo1p: putative membrane protein [Saccharomyces cerevisiae]
23979	ENU07773	ANI61C3047: 23-50 1105..347	592-611	LINAP			g2801701	405	106	1.00E-22	36	22	(AF042379) spindle pole body protein spc97 homolog GCP2 [Homo sapiens] "
23980	ENU07774	ANI61C3850: 117-136 1..334	282-303	LINAP			g4098647	159	85	2.00E-16	43	24	dioxygenase [Arabidopsis thaliana] "
23981	ENU07775	ANI61C311:1 380..679		LINAP			g3540219	705	217	8.00E-56	51	19	(D87686) KIAA0017 protein [Homo sapiens]
23982	ENU07776	ANI61C7345: 61-84 1..597	549-576	LINAP			g2495720	173	69	6.00E-20	35	20	hypothetical protein KIAA0210 ; (D86965) similar to a putative protein coded in Caenorhabditis elegans cosmid B0393. [Homo sapiens]
23983	ENU07777	ANI61C6723: 1583..570		LINAP			g1077415	529	239	2.00E-62	40	31	hypothetical protein YLR357w - yeast (Saccharomyces cerevisiae) ; (U19102) Ylr357wp [Saccharomyces cerevisiae]
23984	ENU07778	ANI61C1952: 43-62 1269..2376	811-829	LINAP			g3915187	902	170	9.00E-49	40	14	probable N-end-recognizing protein (ubiquitin-protein ligase E3 component) (N- recognin) ; ligase [Schizosaccharomyces pombe]
23985	ENU07779	ANI61C9727: 22-46 4681..5583	724-749	LINAP			g3023260	426	115	6.00E-48	48	23	alpha-glucosidase precursor (maltase) ; (D86624) alpha-glucosidase precursor [Spinacia oleracea]
23986	ENU07780	ANI61C7285: 25-48 3265..3862	363-383	LINAP			g116149	297	139	2.00E-32	47	63	G1/S-specific cyclin PCL1 (cyclin HCS26) ; cyclin G1 homolog HCS26 - yeast (Saccharomyces cerevisiae) ; (M73966) G1 cyclin [Saccharomyces cerevisiae] ; (Z71565) ORF YNL289w [Saccharomyces cerevisiae]
23987	ENU07781	ANI61C298:5 891..4773	784-803	LINAP			g2507070	182	65	7.00E-10	31	50	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]

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23988	ENU07782	ANI61C3844: 379..1042	57-76	620-643	LINAP		g1363740	157	76	2.00E-13	36	81	probable membrane protein YLR251w - yeast (Saccharomyces cerevisiae) ; (U20865) Ylr251 wp [Saccharomyces cerevisiae]
23989	ENU07783	ANI61C9748: 23-42	23-42	513-540	LINAP		g3874557	356	166	1.00E-40	45	25	(Z81041) predicted using Genefinder; Similarity to E.coli L-asparaginase (SW:P18840); cDNA EST EMBL:D34586 comes from this gene; cDNA EST EMBL:D35768 comes from this gene; cDNA EST EMBL:D64950 comes from this gene; cDNA EST EMB...
23990	ENU07784	ANI61C6697: 42-61	42-61	799-825	LINAP		g671684	1353	200	1.00E-50	40	32	(U20346) H antigen precursor [Ajellomyces capsulatus]
23991	ENU07785	ANI61C2019: 3617..5527	22-45	443-469	LINAP		g2660584	111	39	0.021			(Y11823) colicin U [Shigella boydii]
23992	ENU07786	ANI61C298:7 839..8331	23-50	440-467	LINAP		g118239	117	52	0.000004	35	53	"dihydrodipicolinate synthase (DHPS) ; (X53993) L-2,3-dihydrodipicolinate synthetase [Corynebacterium glutamicum] "
23993	ENU07787	ANI61C9755: 1197..511	40-59	637-656	LINAP		g550095	296	145	2.00E-34	43	18	(D38310) Boi2p [Saccharomyces cerevisiae]
23994	ENU07788	ANI61C3107: 1458..2133	22-42	621-643	LINAP		g4490979	136	83	2.00E-15			(AL035707) CDA peptide synthetase III [Streptomyces coelicolor]
23995	ENU07789	ANI61C6711: 30-54	30-54	709-730	LINAP		g2739028	115	57	0.000000			(AF023919) PK-120 precursor [Mus musculus]
23996	ENU07790	ANI61C9731: 3450..4811	38-58	436-455	LINAP		g114866	55	57	0.000000	33	49	Magnesium-chelataase 30 KD subunit ; bchO protein - Rhodobacter capsulatus ; (Z11165) 284 aa (30 kD) Mg chelataase subunit [Rhodobacter capsulatus]
23997	ENU07791	ANI61C2060: 600..1	28-50	508-535	LINAP		g2408014	186	106	1.00E-22	33	41	(Z99162) hypothetical protein [Schizosaccharomyces pombe]
23998	ENU07792	ANI61C3860: 2937..774	47-66	789-808	LINAP		g2147662	987	145	3.00E-34	36	12	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium ; (D83643) polyketide synthase [Colletotrichum lagenarium]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23999	ENU07793	ANI61C7926: 2051..472	24-43	804-829	LINAP		g541015	265	32	4			hypothetical protein 471 - Rhizobium leguminosarum ; (X77198) orf471; homologous to NodT [Rhizobium leguminosarum]
24000	ENU07794	ANI61C7335: 2014..2622	22-44	535-554	LINAP		g729344	138	104	4.00E-22			"DLTE protein ; hypothetical protein - Bacillus subtilis ; dltE product[putative cytosolic oxidoreductase [Bacillus subtilis, Peptide, 252 aa] ; (X73124) ipa-1r [Bacillus subtilis] ; (Z99123) alternate gene name: ipa-1r [Bacillus subtilis]"
24001	ENU07795	ANI61C3863: 2806..1	22-45	707-730	LINAP		g2414649	471	116	1.00E-25	29	10	(Z99296) hypothetical protein [Schizosaccharomyces pombe]
24002	ENU07796	ANI61C7355: 1301..2388	22-41	771-790	LINAP		g131777	868	232	3.00E-60	47	24	DNA repair protein RAD13 ; excision repair protein - fission yeast (Schizosaccharomyces pombe) ; (X66795) excision repair protein [Schizosaccharomyces pombe]
24003	ENU07797	ANI61C380:1..376	112-131	330-349	LINAP		g1122901	39	39	0.013			(X94215) MSP8 [Saccharomyces cerevisiae]
24004	ENU07798	ANI61C7962: 1..473	51-70	407-426	LINAP		g1166378	44	108	2.00E-23	36	14	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
24005	ENU07799	ANI61C6708: 1..380	121-140	311-330	LINAP		g3818605	166	68	2.00E-11	44	3	"(AF091251) Ybt peptide/polyketide synthetase HMWP1 [Yersinia pestis] ; (AL031866) ORF68, len=3163 aa, irp1, function=synthesis of siderophore yersiniabactin, product=HMWP1 protein, 97.9% identity in 3163 aa overlap to YEIRPOP_1
24006	ENU07800	ANI61C31:1..949	32-51	804-826	LINAP		g861336	170	75	2.00E-13	40	69	Y.enterocolitica irp1, Fasta scores: opt: 2088, E(): 0 [Yersinia pestis]" (U28943) similar to hydratase-dehydrogenase-epimerase (HDE) [Caenorhabditis elegans]
24007	ENU07801	ANI61C9759: 1593..957	22-44	571-590	LINAP		g1729996	244	112	3.00E-24	38	68	TOXD protein ; (X92391) unique to isolates that make the cyclic peptide HC-toxin [Cochliobolus carbonum]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24008	ENU07802	ANI61C2070: 1017..451			LINAP		g123338	414	63	1.00E-18			3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 (HMG-CoA reductase 2) ; hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) II - yeast (Saccharomyces cerevisiae) ; (M22255) 3-hydroxy-3-methyl glutaryl coenzyme A reductase [Saccharomyces cerevisiae] ; (U22382) Hmg2p: 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase [Saccharomyces cerevisiae]
24009	ENU07803	ANI61C31:35 29..48 29..2201	29-48	796-815	LINAP		g3378265	502	164	9.00E-40	34	63	(AF079317) unknown [Sphingomonas aromaticivorans]
24010	ENU07804	ANI61C3888: 29-52 479..12	29-52	453-479	LINAP		g1730527	110	49	0.000000	35	34	geranylgeranyl transferase type I beta subunit (type I protein geranyl-geranyltransferase beta subunit) (GGTASE-I-beta) ; geranylgeranyl-diphosphate geranylgeranyltransferase (EC 2.5.1.32) I beta chain - rat ; (L24116) geranylgeranyltransferase type I [Rattus norvegicus]
24011	ENU07805	ANI61C7983: 25-52 584..1	25-52	526-552	LINAP		g3913983	340	116	5.00E-36	53	34	probable kynureninase (L-kynurenine hydrolase) ; (U56965) similar to R. norvegicus kynureninase (PIR:PS0370) [Caenorhabditis elegans]
24012	ENU07806	ANI61C7368: 39-66 1492..1	39-66	699-726	LINAP		g3647341	615	92	8.00E-21	43	22	(AL031644) RAD16 nucleotide excision repair protein homolog [Schizosaccharomyces pombe]
24013	ENU07807	ANI61C2088: 53-72 226..1027	53-72	757-781	LINAP		g3668152	142	113	1.00E-24			(AL031764) putative helicase [Schizosaccharomyces pombe]
24014	ENU07808	ANI61C3109: 206-233 384..1066	206-233	633-660	LINAP		g2131257	249	120	1.00E-26	39	47	fumarate reductase (NADH) (EC 1.3.1.6) - yeast (Saccharomyces cerevisiae)
24015	ENU07809	ANI61C3867: 32-51 1045..1509	32-51	455-479	LINAP		g1296845	68	48	0.00005			(X97581) spalt protein [Mus musculus]
24016	ENU07810	ANI61C6714: 22-46 572..872	22-46	459-479	LINAP		g731704	84	46	0.0002	41	42	hypothetical 17.3 KD protein in ERP5-ORC6 intergenic region ; hypothetical protein YHR116w - yeast (Saccharomyces cerevisiae) ; (U00059) Yhr116wp [Saccharomyces cerevisiae]

Gene Description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24017	ENU07811	ANI61C2045: 660..1	22-40	532-559	LINAP		g115689	472	96	5.00E-47	58	55	nuclear protein SNF4 (regulatory protein CAT3) ; CAT3 protein - yeast (Saccharomyces cerevisiae) ; (M21760) regulatory protein CAT3 [Saccharomyces cerevisiae] ; (M30470) SNF4 protein [Saccharomyces cerevisiae] ; (Z72637) ORF YGL115w [Saccharomyces cerevisiae] "(AL031852) valyl-trna synthetase, mitochondrial precursor [Schizosaccharomyces pombe] ; (AL031856) valyl-trna synthetase, mitochondrial precursor [Schizosaccharomyces pombe] " probable sterigmatocystin biosynthesis P450 monooxygenase STCB (cytochrome P450 62) ; (U34740) putative p450 monooxygenase [Emicella nidulans] (AF013216) unknown [Myxococcus xanthus] hypothetical 65.3 KD protein in SUN4-MAS5 intergenic region ; probable membrane protein YNL065w - yeast (Saccharomyces cerevisiae) ; (U12141) membrane protein [Saccharomyces cerevisiae] ; (Z71341) ORF YNL065w [Saccharomyces cerevisiae] cytochrome B5 (AF069765) signal recognition particle 72 [Homo sapiens] ; (AF077019) signal recognition particle 72 [Homo sapiens] probable sucrose utilization protein SUC1 (AB003395) ent-Kaurene synthase [Phaeosphaeria sp. L487]
24018	ENU07812	ANI61C3092: 26-53 4451..5044	26-53	438-461	LINAP		g3738140	516	219	1.00E-56	56	20	
24019	ENU07813	ANI61C9741: 5356..6142			LINAP		g2493391	209	70	2.00E-11	32	26	
24020	ENU07814	ANI61C6714: 23-42 6661..7031	23-42	423-450	LINAP		g2384693	100	31	4.6			
24021	ENU07815	ANI61C2101: 670..1			LINAP		g1730741	143	61	3.00E-12	25	38	
24022	ENU07816	ANI61C3893: 45-64 1669..1973	45-64	450-477	LINAP		g117808	158	81	6.00E-15	48	55	
24023	ENU07817	ANI61C9739: 28-54 4457..2354	28-54	800-819	LINAP		g3243033	251	83	3.00E-15	27	40	
24024	ENU07818	ANI61C7925: 4042..3499			LINAP		g1174472	126	66	1.00E-10	29	35	
24025	ENU07819	ANI61C6769: 22-46 1062..258	22-46	728-754	LINAP		g2443355	207	76	2.00E-13	37	26	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24026	ENU07820	ANI61C2111: 316..685			LINAP		g4038642	265	87	3.00E-20	54	29	(D87063) chitinase [Emericella nidulans]
24027	ENU07821	ANI61C3136: 211-238 328..713	455-479		LINAP		g2239197	137	80	8.00E-15	32	76	(Z97209) ureidoglycolate hydrolase [Schizosaccharomyces pombe]
24028	ENU07822	ANI61C9770: 37-57 3123..3644	468-495		LINAP		g1730641	159	146	1.00E-34	48	26	hypothetical 65.0 KD protein in MET2-SEC2 intergenic region ; probable membrane protein YNL275w - yeast (Saccharomyces cerevisiae) ; (Z71551) ORF YNL275w [Saccharomyces cerevisiae]
24029	ENU07823	ANI61C7336: 52-71 1..3069	807-829		LINAP		g119830	2976	299	1.00E-80	52	15	"fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41] ; fatty-acid synthase (EC 2.3.1.85) - Penicillium griseofulvum ; (M37461) FAS2 protein [Penicillium patulum] " (AC003952) putative histidine kinase [Arabidopsis thaliana] (AF016696) peptide synthetase module [Streptomyces fradiae]
24030	ENU07824	ANI61C2130: 22-43 581..97	420-439		LINAP		g2708752	74	60	0.000000			DNA polymerase alpha/PRIMASE associated subunit (P86 subunit) ; probable membrane protein YBL035c - yeast (Saccharomyces cerevisiae) ; (X74738) ORF YBL0415 [Saccharomyces cerevisiae] ; (Z35796) ORF YBL035c [Saccharomyces cerevisiae] ; ORF YBL0415 [Saccharomyces cerevisiae]
24031	ENU07825	ANI61C3134: 101-127 2089..1338	706-731		LINAP		g2738765	82	102	2.00E-21			hypothetical 50.2 KD protein in CPT1-SPC98 intergenic region ; probable tyrosine phosphatase YNL128w - yeast (Saccharomyces cerevisiae) ; (Z46843) tyrosine phosphatase (putative) [Saccharomyces cerevisiae] ; (Z71404) ORF YNL128w [Saccharomyces cerevisiae]
24032	ENU07826	ANI61C9760: 22-42 741..1	618-639		LINAP		g585063	415	150	1.00E-35	39	34	
24033	ENU07827	ANI61C6776: 35-54 1436..1979	472-494		LINAP		g1730775	98	42	0.000000	35	32	
24034	ENU07828	ANI61C3146: 24-42 1603..2092	264-283		LINAP		g3559814	312	118	2.00E-26	58	16	transketolase 1 [Capsicum annuum]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24047	ENU07842	ANI61C1027 3:250..1270			GTBX	"AFUc01302, AFUc18982, FGRc04116"				"1.6e-111, 6.2e-14, 1.2e-30"			
24048	ENU07843	ANI61C1027 4:2845..3490			GTBX	"AFUc05575, AFUc07542"				"4.3e-09, 9.4e-21"			
24049	ENU07844	ANI61C1027 5:2551..4131			GTBX	"AFUc01701, AFUc09710, AFUc09710, AFUc12211, AFUc20787, AFUc21939, Z71256"				"7.0e-23, 3.3e-23, 3.9e-14, 3.9e-24, 1.9e-13, 3.3e-25, 2.7e-07"			
24050	ENU07845	ANI61C1027 9:79..1101			GTBX	FGRc22675				3.9E-33			
24051	ENU07846	ANI61C1481: 592..54			GTBX	"AFUc10211, AFUc15427"				"4.2e-36, 6.7e-28"			
24052	ENU07847	ANI61C1487: 963..1571			GTBX	"AFUc04386, CALc02388"				"3.3e-81, 1.6e-08"			
24053	ENU07848	ANI61C1489: 487..281			GTBX	AFUc14845				8.1E-30			
24054	ENU07849	ANI61C1028 0:1900..466			GTBX	"AFUc01505, AFUc06388, FGRc05792, FGRc08715, FGRc10632"				"7.8e-46, 1.3e-45, 1.0e-20, 3.2e-18, 9.6e-14"			
24055	ENU07850	ANI61C1028 2:1207..1860			GTBX	AFUc14473				1.3E-129			
24056	ENU07851	ANI61C1028 5:548..831			GTBX	"CALc03391, Y13137"				"9.0e-29, 6.1e-39"			
24057	ENU07852	ANI61C1028 7:1684..2097			GTBX	U00092				6.0e-55			

Table 2. Contigs

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24058	ENU07853	ANI61C1493:117..1265			GTBX	"AFUc19753, FGRC23159"				"2.0e-25, 7.6e-27"			
24059	ENU07854	ANI61C1495:294..538			GTBX	U00094				1.6e-51			
24060	ENU07855	ANI61C1496:741..115			GTBX	AFUc03226				1.3E-38			
24061	ENU07856	ANI61C320:251..612			GTBX	AFUc12957				1.1E-40			
24062	ENU07857	ANI61C321:7229..6601			GTBX	AFUc21833				5E-31			
24063	ENU07858	ANI61C322:3260..3635			GTBX	"AFUc20332, FGRC09045"				"4.5e-25, 5.0e-15"			
24064	ENU07859	ANI61C327:400..34			GTBX	FGRC11552				3E-22			
24065	ENU07860	ANI61C10296:2669..18			GTBX	"AFUc15183, CALc05935"				"1.6e-85, 5.4e-262"			
24066	ENU07861	ANI61C10296:11566..12246			GTBX	AFUc15911				7E-93			
24067	ENU07862	ANI61C10297:23..1444			GTBX	AFUc15769				9.4E-113			
24068	ENU07863	ANI61C10299:1537..3212			GTBX	"AFUc21263, FGRC09112"				"3.8e-55, 6.6e-63"			
24069	ENU07864	ANI61C10299:4892..3860			GTBX	AFUc12138				5.7E-25			
24070	ENU07865	ANI61C10299:5928..6774			GTBX	AFUc03113				5.7E-64			
24071	ENU07866	ANI61C1:30..683			GTBX	AFUc09360				4.1E-27			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24086	ENU07881	ANI61C379:4 245..5557			GTBX	"AFUc04762, FGRc21465"				"7.2e-41, 2.0e-37"			
24087	ENU07882	ANI61C379:7 058..6858			GTBX	AFUc15378				1.4E-23			
24088	ENU07883	ANI61C382:1 430..510			GTBX	"AFUc10214, AFUc13687"				"1.0e-56, 4.9e-33"			
24089	ENU07884	ANI61C383:3 030..3578			GTBX	AFUc06191				1.1E-56			
24090	ENU07885	ANI61C7223: 6059..5046			GTBX	"CALc05044, FGRc18203"				"2.8e-67, 1.6e-41"			
24091	ENU07886	ANI61C395:1 29..502			GTBX	FGRc01389				7.2E-34			
24092	ENU07887	ANI61C7231: 571..130			GTBX	AFUc06018				5.9E-32			
24093	ENU07888	ANI61C7232: 1188..2754			GTBX	"AFUc15564, AFUc20293"				"2.5e-99, 1.8e-34"			
24094	ENU07889	ANI61C7232: 6257..6705			GTBX	AFUc02538				1E-33			
24095	ENU07890	ANI61C6504: 15..1182			GTBX	AFUc12291				3.4E-21			
24096	ENU07891	ANI61C7234: 1359..273			GTBX	"AFUc07075, AFUc15048"				"2.8e-85, 4.2e-17"			
24097	ENU07892	ANI61C7236: 3414..1523			GTBX	"AFUc04239, AFUc09737"				"7.5e- 119, 1.4e-36"			
24098	ENU07893	ANI61C7242: 1515..1201			GTBX	FGRc19758				1.1E-23			
24099	ENU07894	ANI61C6518: 848..1501			GTBX	AFUc09603				1.7E-54			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24100	ENU07895	ANI61C7249: 1489..574			GTBX	"FGRc17352, U00092"				"9.7e-37, 2.3e-30"			
24101	ENU07896	ANI61C6521: 103..759			GTBX	"AFUc06725, AFUc09341"				"2.4e-12, 1.1e-35"			
24102	ENU07897	ANI61C7251: 609..10			GTBX	AFUc13794				8.5E-76			
24103	ENU07898	ANI61C7252: 785..43			GTBX	"AFUc11055, FGRc22632"				"3.1e-95, 4.2e-07"			
24104	ENU07899	ANI61C6526: 4472..3329			GTBX	"AFUc00779, FGRc05727, FGRc22503"				"2.2e-24, 2.1e-14, 3.0e-17"			
24105	ENU07900	ANI61C6527: 6158..6573			GTBX	"AFUc12900, FGRc14925"				"2.5e-164, 9.5e-14"			
24106	ENU07901	ANI61C6532: 3..497			GTBX	AFUc01942				2.9E-60			
24107	ENU07902	ANI61C6532: 3956..6787			GTBX	"AFUc05806, AFUc12778, AFUc19750"				"2.6e-52, 5.2e-157, 1.0e-21"			
24108	ENU07903	ANI61C6535: 4190..5827			GTBX	"AFUc16901, FGRc10006"				"6.8e-44, 4.9e-23"			
24109	ENU07904	ANI61C6535: 10281..9997			GTBX	AFUc03224				3.4E-43			
24110	ENU07905	ANI61C5807: 670..1293			GTBX	"AFUc08318, AFUc08318, FGRc09465"				"3.6e-82, 4.6e-80, 2.3e-35"			
24111	ENU07906	ANI61C5808: 514..1299			GTBX	"AFUc04514, AFUc13919, CALc05514, D50167"				"1.2e-76, 1.0e-07, 4.8e-25, 4.5e-08"			
24112	ENU07907	ANI61C5809: 284..6			GTBX	AFUc16862				3.8E-27			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24113	ENU07908	ANI61C5810: 819..47			GTBX	"AFUc08467, CALc05923"				"4.4e-09, 8.3e-56"			
24114	ENU07909	ANI61C6540: 3119..3417			GTBX	AFUc08906				9E-44			
24115	ENU07910	ANI61C5813: 460..1074			GTBX	AFUc12201				7.9E-95			
24116	ENU07911	ANI61C7273: 960..2083			GTBX	AFUc10281				1.1E-47			
24117	ENU07912	ANI61C7274: 1136..206			GTBX	AFUc03210				2.9E-57			
24118	ENU07913	ANI61C7276: 3527..4341			GTBX	"AFUc01802, FGRC10582"				"1.6e-22, 1.3e-15"			
24119	ENU07914	ANI61S207:5 43..121			GTBX	AFUc07853				3.8E-25			
24120	ENU07915	ANI61C7280: 335..1938			GTBX	"FGRC08244, FGRC16187"				"1.3e-71, 2.0e-46"			
24121	ENU07916	ANI61C6552: 3134..4669			GTBX	"AFUc13978, AFUc16716, AFUc19617, FGRC15557"				"1.1e-31, 1.4e-29, 2.0e-44, 6.2e-18"			
24122	ENU07917	ANI61C6553: 3869..4420			GTBX	AFUc11116				5.8E-30			
24123	ENU07918	ANI61C6556: 441..97			GTBX	AFUc13317				1.2E-36			
24124	ENU07919	ANI61C7285: 916..1315			GTBX	FGRC02595				1.9E-36			
24125	ENU07920	ANI61C7285: 7900..8248			GTBX	AFUc15172				4.4E-69			
24126	ENU07921	ANI61C5829: 736..359			GTBX	AFUc08971				4.2E-34			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24127	ENU07922	ANI61S219:4 84..9			GTBX	AFUc08358				1.5E-60			
24128	ENU07923	ANI61C5831: 903..18			GTBX	AFUc14499				6.3E-77			
24129	ENU07924	ANI61C7290: 909..336			GTBX	Y13134				3.0e-28			
24130	ENU07925	ANI61C6562: 1020..89			GTBX	"AFUc01328, AFUc04061"				"6.1e-55, 3.1e-53"			
24131	ENU07926	ANI61C5834: 536..1960			GTBX	CALc03151				8.9E-171			
24132	ENU07927	ANI61C5835: 1327..116			GTBX	"AFUc02187, AFUc12580, AFUc16794"				"1.4e-14, 1.9e-07, 4.2e-61"			
24133	ENU07928	ANI61C6564: 16..965			GTBX	"AFUc16593, FGRc03157"				"4.2e-43, 1.2e-11"			
24134	ENU07929	ANI61C5836: 693..5			GTBX	"CALc04906, FGRc04099"				"2.4e-48, 8.5e-59"			
24135	ENU07930	ANI61C5837: 3117..648			GTBX	AFUc14040				8.4E-26			
24136	ENU07931	ANI61C7298: 592..8			GTBX	CALc06027				3E-39			
24137	ENU07932	ANI61C6570: 951..739			GTBX	CALc06157				1.4E-65			
24138	ENU07933	ANI61C6579: 931..141			GTBX	"AFUc02825, AFUc16044"				"9.5e-21, 9.7e-09"			
24139	ENU07934	ANI61C5852: 88..835			GTBX	CALc05688				3.7E-57			
24140	ENU07935	ANI61C5852: 2281..1223			GTBX	"AFUc07544, AFUc08833"				"7.4e-09, 2.7e-29"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24141	ENU07936	ANI61C5853:1007..1811			GTBX	"AFUc10318, AFUc15156"				"4.9e-73, 1.7e-72"			
24142	ENU07937	ANI61C6585:892..1140			GTBX	"AFUc05311, AFUc05311"				"1.7e-47, 1.7e-73"			
24143	ENU07938	ANI61C6588:1804..14			GTBX	"AFUc08190, AFUc11152, AFUc15526, FGRc05298"				"1.2e-09, 2.1e-62, 3.6e-10, 1.1e-08"			
24144	ENU07939	ANI61C5865:538..89			GTBX	FGRc10441				1.7E-47			
24145	ENU07940	ANI61C6598:1573..2608			GTBX	"AFUc01830, FGRc04488"				"2.3e-50, 9.2e-32"			
24146	ENU07941	ANI61S8:287..42			GTBX	AFUc04879				2.1E-32			
24147	ENU07942	ANI61C5885:361..1250			GTBX	AFUc15363				3.4E-94			
24148	ENU07943	ANI61C5886:756..40			GTBX	AFUc19850				9.8E-58			
24149	ENU07944	ANI61C5888:643..1866			GTBX	FGRc11984				1.5E-95			
24150	ENU07945	ANI61S2026:43..360			GTBX	AFUc10511				2.8E-36			
24151	ENU07946	ANI61S1309:546..16			GTBX	AFUc06122				3.2E-88			
24152	ENU07947	ANI61C2202:737..1023			GTBX	"AFUc10677, Y13136"				"1.8e-20, 3.0e-102"			
24153	ENU07948	ANI61C2209:1288..64			GTBX	"AFUc17374, AFUc20460"				"1.1e-59, 9.1e-31"			
24154	ENU07949	ANI61C1100:0:8262..9041			GTBX	AFUc14297				3.3E-45			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24155	ENU07950	ANI61C1100 4:1954..1302			GTBX	AFUc14982				1E-161			
24156	ENU07951	ANI61C2214: 1695..1099			GTBX	AFUc10709				1.3E-47			
24157	ENU07952	ANI61C2216: 54..1022			GTBX	Z71256				9.0e-15			
24158	ENU07953	ANI61C1101 0:1243..2169			GTBX	"AFUc14408, FGRc07288"				"4.0e-33, 2.4e-38"			
24159	ENU07954	ANI61C2220: 29..773			GTBX	AFUc02313				8.5E-22			
24160	ENU07955	ANI61C1102 3:79..1083			GTBX	"AFUc06153, AFUc21355, FGRc08305"				"3.7e-61, 9.8e-54, 4.2e-07" 6.5E-57			
24161	ENU07956	ANI61C2235: 1966..1466			GTBX	AFUc06983							
24162	ENU07957	ANI61C1103 0:300..2243			GTBX	"AFUc15517, AFUc20784, FGRc15017"				"2.6e-20, 4.8e-15, 3.1e-29" "1.0e-22, 8.0e-25"			
24163	ENU07958	ANI61C1103 0:8409..9713			GTBX	"AFUc06388, FGRc05792"				2.9E-51			
24164	ENU07959	ANI61C1103 1:1655..2023			GTBX	AFUc13932				2.7E-50			
24165	ENU07960	ANI61C1103 2:497..48			GTBX	AFUc11402							
24166	ENU07961	ANI61C1030 4:273..800			GTBX	AFUc15094				5.6E-72			
24167	ENU07962	ANI61C1030 6:613..14			GTBX	AFUc13032				4.4E-37			
24168	ENU07963	ANI61C1103 7:5775..6531			GTBX	AFUc07195				7E-57			

GenBank Database

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24169	ENU07964	ANI61C1103 8:14225..12770			GTBX	"AFUc09489, FGRc09616"				"9.0e-26, 3.6e-17"			
24170	ENU07965	ANI61S1346: 92..435			GTBX	AFUc02348				1.4E-44			
24171	ENU07966	ANI61C1511: 378..1139			GTBX	U00094				5.2e-38			
24172	ENU07967	ANI61C2242: 2406..1912			GTBX	AFUc03452				8.1E-49			
24173	ENU07968	ANI61C1514: 220..815			GTBX	AFUc15554				1.7E-79			
24174	ENU07969	ANI61C1518: 1333..817			GTBX	"AFUc13493, FGRc25564"				"6.5e-23, 4.9e-25"			
24175	ENU07970	ANI61C2249: 68..817			GTBX	AFUc08878				3.5E-79			
24176	ENU07971	ANI61C1031 0:1335..71			GTBX	AFUc09721				3.6E-27			
24177	ENU07972	ANI61C1104 0:2002..2735			GTBX	AFUc09896				3.5E-52			
24178	ENU07973	ANI61C1104 1:851..1973			GTBX	AFUc10517				2.5E-94			
24179	ENU07974	ANI61C1031 3:385..29			GTBX	FGRc07645				1.9E-21			
24180	ENU07975	ANI61C1104 5:39..677			GTBX	U00094				6.2e-38			
24181	ENU07976	ANI61C1104 6:529..740			GTBX	AFUc10641				6.5E-39			
24182	ENU07977	ANI61C1521: 3457..2237			GTBX	AFUc12939				2.7E-101			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24183	ENU07978	ANI61C1525:1163..813			GTBX	FGRc04252				2.1E-23			
24184	ENU07979	ANI61C2256:1738..606			GTBX	"AFUc03478, AFUc06959, FGRc11102"				"5.3e-61, 1.4e-13, 1.6e-68"			
24185	ENU07980	ANI61C1032 4:1456..2640			GTBX	AFUc06432				5.6E-40			
24186	ENU07981	ANI61C1032 4:6683..7378			GTBX	AFUc03858				1.8E-26			
24187	ENU07982	ANI61C1105 7:854..3			GTBX	AFUc15404				1.2E-104			
24188	ENU07983	ANI61C1105 8:1235..3139			GTBX	"AFUc10292, CALc04898"				"1.7e-140, 3.7e-15"			
24189	ENU07984	ANI61C2264:819..487			GTBX	AFUc14213				4.3E-22			
24190	ENU07985	ANI61C2266:678..1117			GTBX	AFUc09002				2.9E-60			
24191	ENU07986	ANI61C1538:1527..2143			GTBX	FGRc13890				2.3E-55			
24192	ENU07987	ANI61C1106 5:1308..25			GTBX	"AFUc01902, CALc06224"				"2.0e-49, 2.4e-36"			
24193	ENU07988	ANI61C1033 8:1068..1298			GTBX	AFUc15802				5.7E-81			
24194	ENU07989	ANI61C2274:104..352			GTBX	FGRc17081				5.7E-24			
24195	ENU07990	ANI61C2279:947..35			GTBX	AFUc12999				3.7E-57			
24196	ENU07991	ANI61C1107 3:10825..9952			GTBX	AFUc08864				1.6E-40			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24197	ENU07992	ANI61C1034 6:148..474			GTBX	AFUc15190				5.2E-32			
24198	ENU07993	ANI61C1107 6:735..40			GTBX	FGRc11607				9.9E-62			
24199	ENU07994	ANI61C2280: 1521..418			GTBX	"AFUc22243, Z71256"				"1.1e-80, 3.3e-65"			
24200	ENU07995	ANI61C1554: 1454..495			GTBX	"AFUc15791, CALc05767"				"1.1e-89, 9.6e-28"			
24201	ENU07996	ANI61C1556: 505..2120			GTBX	"FGRc16102, U00091"				"3.0e-18, 6.1e-13"			
24202	ENU07997	ANI61C1557: 8377..8816			GTBX	"AFUc10195, Y13137"				"2.6e-29, 3.3e-19"			
24203	ENU07998	ANI61C2286: 63..469			GTBX	AFUc19350				1.8E-29			
24204	ENU07999	ANI61C2287: 3657..2752			GTBX	AFUc21287				1.7E-22			
24205	ENU08000	ANI61C1558: 241..1075			GTBX	AFUc07571				1.8E-111			
24206	ENU08001	ANI61C1108 2:2..355			GTBX	AFUc11431				7.8E-49			
24207	ENU08002	ANI61S1390: 27..413			GTBX	AFUc00871				4.2E-54			
24208	ENU08003	ANI61C1035 4:586..266			GTBX	AFUc14370				1E-38			
24209	ENU08004	ANI61C1561: 633..1091			GTBX	"FGRc12428, FGRc23250"				"6.2e-17, 1.3e-26"			
24210	ENU08005	ANI61C1563: 759..984			GTBX	AFUc12486				1.4E-59			

Gene annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24211	ENU08006	ANI61C1564:425..1061			GTBX	"AFUc03100, AFUc08293"				"1.6e-71, 1.0e-71"			
24212	ENU08007	ANI61C1566:1921..1217			GTBX	AFUc06344				1.5E-31			
24213	ENU08008	ANI61C10362:706..1638			GTBX	AFUc05986				2.1E-64			
24214	ENU08009	ANI61C10363:84..749			GTBX	AFUc14403				5.9E-76			
24215	ENU08010	ANI61C11093:666..283			GTBX	AFUc02155				7.1E-43			
24216	ENU08011	ANI61C11098:5774..6408			GTBX	"AFUc02174, AFUc07223"				"3.6e-30, 1.4e-64"			
24217	ENU08012	ANI61C1571:1373..765			GTBX	AFUc09738				2.6E-96			
24218	ENU08013	ANI61C1572:1..528			GTBX	AFUc12035				6.1E-42			
24219	ENU08014	ANI61C1575:538..1212			GTBX	AFUc17343				5.4E-29			
24220	ENU08015	ANI61C404:2381..3391			GTBX	AFUc10663				1.6E-86			
24221	ENU08016	ANI61C404:5543..4664			GTBX	AFUc05891				3.5E-65			
24222	ENU08017	ANI61C409:1650..41			GTBX	"AFUc07919, AFUc13887, AFUc14801, AFUc20578"				"3.7e-46, 4.4e-36, 1.0e-15, 2.9e-59"			
24223	ENU08018	ANI61C1580:532..1125			GTBX	AFUc13632				1.9E-52			
24224	ENU08019	ANI61C1582:909..3			GTBX	Z71257				2.9E-22			

Accession

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24225	ENU08020	ANI61C1586:787..1352			GTBX	AFUc13343				3.2E-39			
24226	ENU08021	ANI61C1038 0:3189..3954			GTBX	AFUc16966				4.2E-32			
24227	ENU08022	ANI61C419:2 8..469			GTBX	FGRc26357				1.1E-49			
24228	ENU08023	ANI61C1038 4:682..2			GTBX	AFUc15000				8.7E-94			
24229	ENU08024	ANI61C1038 6:428..6			GTBX	AFUc14146				1.9E-37			
24230	ENU08025	ANI61C1038 7:3270..4847			GTBX	"AFUc04379, AFUc12739"				"1.9e-45, 5.7e-53"			
24231	ENU08026	ANI61C1598:479..11			GTBX	AFUc16619				4.3E-35			
24232	ENU08027	ANI61C1039 7:1214..133			GTBX	"AFUc06152, AFUc17696, CALc05205"				"1.1e-28, 2.2e-12, 1.3e-46"			
24233	ENU08028	ANI61C438:2 608..906			GTBX	"AFUc07197, AFUc11134, AFUc11728, AFUc12186"				"5.1e-14, 1.1e-15, 1.4e-14, 1.3e-105"			
24234	ENU08029	ANI61C439:9 124..9705			GTBX	AFUc01048				6E-60			
24235	ENU08030	ANI61C8000:994..2			GTBX	"AFUc02858, U00092"				"2.8e-11, 6.6e-93"			
24236	ENU08031	ANI61C8004:608..3			GTBX	AFUc19180				8.2E-24			
24237	ENU08032	ANI61C8006:514..1077			GTBX	AFUc13623				5.3E-40			

GenBank

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24238	ENU08033	ANI61C440:3446..3919			GTBX	AFUc17537				3.9E-64			
24239	ENU08034	ANI61C442:556..131			GTBX	AFUc21017				6.4E-22			
24240	ENU08035	ANI61C445:716..1232			GTBX	GY13139				5.9e-57			
24241	ENU08036	ANI61C449:266..1975			GTBX	AFUc15617				1.4E-206			
24242	ENU08037	ANI61C8012:1970..190			GTBX	AFUc15379				5.1E-111			
24243	ENU08038	ANI61C8013:1851..3360			GTBX	"AFUc07084, AFUc22432, CALc06078, Y13135"				"4.8e-66, 2.1e-41, 1.1e-54, 5.7e-37" 2.5E-36			
24244	ENU08039	ANI61C8020:5..382			GTBX	AFUc13797				6.6E-63			
24245	ENU08040	ANI61C8021:3545..2350			GTBX	AFUc13604							
24246	ENU08041	ANI61C8026:38..1772			GTBX	"AFUc15772, AFUc21150, FGRc16885"				"4.9e-143, 2.0e-13, 2.5e-11" 1.3E-47			
24247	ENU08042	ANI61C8029:16..570			GTBX	AFUc21824				1.6E-38			
24248	ENU08043	ANI61C467:5371..6057			GTBX	AFUc04398				2.7E-59			
24249	ENU08044	ANI61C8031:823..117			GTBX	AFUc11877				4.1E-24			
24250	ENU08045	ANI61C7308:36..415			GTBX	AFUc00888							

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24251	ENU08046	ANI61C477:6 30..1			GTBX	AFUc15892				1.5E-52			
24252	ENU08047	ANI61C7311: 163..582			GTBX	"AFUc04986, AFUc09264"				"5.4e-16, 5.2e-55"			
24253	ENU08048	ANI61C8044: 326..1058			GTBX	AFUc14880				5E-46			
24254	ENU08049	ANI61C7315: 1841..3604			GTBX	"AFUc12313, AFUc19899"				"2.1e-43, 2.9e-37"			
24255	ENU08050	ANI61C7317: 1666..56			GTBX	"AFUc11411, CALc06214, Y13135"				"8.6e- 115, 1.2e-67, 1.3e-42" 5.4E-21			
24256	ENU08051	ANI61C8047: 5242..4733			GTBX	AFUc15695				1.9E-80			
24257	ENU08052	ANI61C7318: 655..1047			GTBX	"AFUc18123, Y13139"				"6.8e-21, 1.2e-09"			
24258	ENU08053	ANI61C489:4 57..3			GTBX	AFUc13648							
24259	ENU08054	ANI61C8051: 1747..518			GTBX	"CALc04459, CALc04459"				"1.4e-61, 3.0e-62"			
24260	ENU08055	ANI61C7323: 785..241			GTBX	AFUc19691				7E-56			
24261	ENU08056	ANI61C8052: 733..2502			GTBX	"AFUc00069, AFUc16115, CALc04031"				"2.8e-71, 6.0e-34, 7.0e-55"			
24262	ENU08057	ANI61C8053: 610..182			GTBX	AFUc10161				1.7E-21			
24263	ENU08058	ANI61C8055: 2135..174			GTBX	"AFUc11740, AFUc12687, AFUc14731, FGRc23552"				"5.7e-57, 4.0e-21, 5.0e-19, 6.6e-14"			

BLAST Results

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24264	ENU08059	ANI61C8057: 52..420			GTBX	AFUc08475				2E-49			
24265	ENU08060	ANI61C7329: 594..1704			GTBX	"AFUc01746, AFUc02096"				"1.2e-27, 3.5e-52"			
24266	ENU08061	ANI61C492:5 7..884			GTBX	AFUc13259				3.6E-135			
24267	ENU08062	ANI61C499:1 160..732			GTBX	AFUc09357				1.1E-68			
24268	ENU08063	ANI61C7330: 143..2372			GTBX	"AFUc13887, AFUc14801, FGRc09062, FGRc10889, FGRc21319"				"2.5e-43, 1.3e-13, 1.6e-45, 5.2e-99, 1.5e-10"			
24269	ENU08064	ANI61C7330: 3367..4124			GTBX	"AFUc05528, FGRc11979"				"6.7e-27, 3.8e-13"			
24270	ENU08065	ANI61C7331: 4011..2258			GTBX	"AFUc03996, AFUc06614, AFUc15699, AFUc15879"				"1.6e-21, 3.9e-15, 3.4e-19, 1.6e-43"			
24271	ENU08066	ANI61C6607: 1409..2016			GTBX	"AFUc10110, AFUc19217"				"5.5e-22, 1.4e-48"			
24272	ENU08067	ANI61C8066: 866..1393			GTBX	"AFUc11731, CALc05890"				"6.5e-121, 3.7e-112"			
24273	ENU08068	ANI61C7340: 450..7			GTBX	Y13134				9.1e-28			
24274	ENU08069	ANI61C6611: 98..870			GTBX	AFUc07093				4.5E-60			
24275	ENU08070	ANI61C8071: 516..13			GTBX	AFUc09728				1.8E-53			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24276	ENU08071	ANI61C6614: 1400..874			GTBX	AFUc15221				1.2E-142			
24277	ENU08072	ANI61C8074: 5126..4678			GTBX	AFUc12456				2.7E-29			
24278	ENU08073	ANI61C6616: 377..1089			GTBX	"AFUc05353, AFUc19936"				"1.7e-54, 4.0e-12"			
24279	ENU08074	ANI61C6617: 4827..5366			GTBX	Z47047				1.0e-125			
24280	ENU08075	ANI61C7350: 2489..1882			GTBX	FGRc09585				1.6E-22			
24281	ENU08076	ANI61C8082: 1136..2144			GTBX	AFUc15770				3.9E-135			
24282	ENU08077	ANI61C6626: 6507..7319			GTBX	AFUc10550				2.5E-151			
24283	ENU08078	ANI61C6627: 585..838			GTBX	AFUc03450				3.9E-50			
24284	ENU08079	ANI61C7356: 2072..2291			GTBX	"CALc06084, Y13137"				"4.6e-49, 8.3e-235"			
24285	ENU08080	ANI61C8087: 2424..1939			GTBX	AFUc07211				4.7E-51			
24286	ENU08081	ANI61C5902: 1004..261			GTBX	AFUc12988				3.5E-72			
24287	ENU08082	ANI61C8090: 5575..6094			GTBX	FGRc12352				1E-36			
24288	ENU08083	ANI61C7361: 1567..2745			GTBX	AFUc09895				6.4E-117			
24289	ENU08084	ANI61C5903: 811..368			GTBX	AFUc15950				2.6E-157			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24290	ENU08085	ANI61C5904: 765..25			GTBX	"AFUc00773, AFUc11153"				"7.1e-16, 1.9e-29"			
24291	ENU08086	ANI61C6635: 944..282			GTBX	AFUc02614				5.8E-36			
24292	ENU08087	ANI61C7364: 1168..2132			GTBX	"AFUc01872, FGRc01926"				"1.0e-136, 2.4e-24"			
24293	ENU08088	ANI61C5907: 1099..443			GTBX	AFUc02783				2.1E-34			
24294	ENU08089	ANI61C6639: 306..7			GTBX	AFUc10259				3.7E-24			
24295	ENU08090	ANI61C5910: 5311..6464			GTBX	AFUc09815				2.6E-69			
24296	ENU08091	ANI61C7370: 369..1672			GTBX	AFUc10420				5E-119			
24297	ENU08092	ANI61C5913: 489..1			GTBX	"FGRc02041, U00092"				"6.1e-12, 6.1e-12"			
24298	ENU08093	ANI61C6644: 1478..646			GTBX	"AFUc06809, AFUc15344"				"4.6e-09, 4.4e-98"			
24299	ENU08094	ANI61C5918: 499..18			GTBX	FGRc07459				6E-57			
24300	ENU08095	ANI61C6649: 1057..2094			GTBX	AFUc15961				2.5E-39			
24301	ENU08096	ANI61C7379: 962..28			GTBX	AFUc08907				1.2E-21			
24302	ENU08097	ANI61C5922: 1491..291			GTBX	"CALc06174, FGRc08383"				"4.5e-31, 4.8e-31"			
24303	ENU08098	ANI61C7381: 300..1060			GTBX	"AFUc10566, AFUc10566"				"3.6e-30, 9.6e-41"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24304	ENU08099	ANI61C6652: 2208..1501			GTBX	AFUc09205				3.9E-50			
24305	ENU08100	ANI61C7387: 575..3			GTBX	FGRc10619				4.7E-31			
24306	ENU08101	ANI61C7387: 1279..1652			GTBX	"AFUc15408, AFUc21306"				"5.7e-19, 1.5e-31"			
24307	ENU08102	ANI61C7389: 1326..60			GTBX	CALc05599				4.8E-124			
24308	ENU08103	ANI61C5930: 3876..5599			GTBX	"AFUc13125, AFUc17372"				"4.4e-183, 1.6e-68"			
24309	ENU08104	ANI61C6660: 2123..319			GTBX	"AFUc00228, AFUc00481, AFUc02234"				"5.3e-27, 1.0e-27, 9.8e-33"			
24310	ENU08105	ANI61C7390: 1588..2441			GTBX	Y13139				1.0e-127			
24311	ENU08106	ANI61C6661: 3226..5249			GTBX	"AFUc12095, FGRc15027"				"2.5e-198, 4.1e-29"			
24312	ENU08107	ANI61C6662: 5034..5514			GTBX	AFUc09341				2.9E-28			
24313	ENU08108	ANI61C7393: 703..293			GTBX	AFUc15863				2.6E-52			
24314	ENU08109	ANI61C5938: 198..1256			GTBX	AFUc12786				3.3E-79			
24315	ENU08110	ANI61C6670: 1277..1597			GTBX	AFUc00716				1.4E-36			
24316	ENU08111	ANI61C5943: 623..93			GTBX	AFUc15520				1.4E-45			
24317	ENU08112	ANI61C6675: 830..254			GTBX	CALc04506				7E-39			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24318	ENU08113	ANI61C5946: 384..1079			GTBX	AFUc13556				1.7E-75			
24319	ENU08114	ANI61C5952: 520..28			GTBX	AFUc17155				3.9E-41			
24320	ENU08115	ANI61C5954: 55..1083			GTBX	"AFUc03799, AFUc10276"				"3.7e-57, 7.3e-09"			
24321	ENU08116	ANI61C6685: 43..903			GTBX	"CALc04792, FGRC09020, U00093"				"2.4e-53, 2.0e-32, 7.8e-49"			
24322	ENU08117	ANI61C5957: 1663..1999			GTBX	AFUc02793				2.2E-30			
24323	ENU08118	ANI61C6686: 4251..5701			GTBX	AFUc15881				6.9E-80			
24324	ENU08119	ANI61C5961: 1203..511			GTBX	AFUc01030				1.1E-38			
24325	ENU08120	ANI61C5964: 1000..1293			GTBX	AFUc15826				1.8E-25			
24326	ENU08121	ANI61C5966: 658..980			GTBX	AFUc14716				8.1E-39			
24327	ENU08122	ANI61C5968: 1055..834			GTBX	Z71256				1.4e-23			
24328	ENU08123	ANI61C5975: 178..611			GTBX	AFUc02362				1.6E-60			
24329	ENU08124	ANI61C5976: 1505..86			GTBX	"AFUc15353, CALc06066, FGRC02066"				"8.2e-52, 6.3e-34, 5.0e-73"			
24330	ENU08125	ANI61S2111: 116..469			GTBX	FGRC08800				3.9E-32			
24331	ENU08126	ANI61C5984: 211..731			GTBX	AFUc15082				4.1E-55			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24332	ENU08127	ANI61C5988:1524..225			GTBX	"AFUc15870, AFUc18615"				"1.1e-51, 1.5e-32"			
24333	ENU08128	ANI61C3014:1868..825			GTBX	AFUc12007				3.5E-33			
24334	ENU08129	ANI61C3015:384..1558			GTBX	"AFUc06441, AFUc18928, FGRC12021, FGRC13993"				"1.4e-23, 2.4e-39, 1.4e-23, 4.5e-17"			
24335	ENU08130	ANI61C5995:1002..463			GTBX	"AFUc15651, AFUc15651"				"1.3e-66, 4.5e-89"			
24336	ENU08131	ANI61S2128:94..537			GTBX	AFUc07714				1.3E-44			
24337	ENU08132	ANI61C3022:992..720			GTBX	AFUc07125				7E-30			
24338	ENU08133	ANI61S2133:44..472			GTBX	AFUc22602				1.6E-46			
24339	ENU08134	ANI61C2304:560..132			GTBX	AFUc07438				1.3E-32			
24340	ENU08135	ANI61C3035:910..296			GTBX	"AFUc11981, FGRC10039"				"6.2e-40, 1.6e-09"			
24341	ENU08136	ANI61C3037:579..7			GTBX	AFUc09927				7.5E-56			
24342	ENU08137	ANI61C2309:974..363			GTBX	"AFUc03406, AFUc05614, AFUc08898, CALc05491"				"2.9e-54, 5.7e-54, 1.4e-19, 8.4e-09"			
24343	ENU08138	ANI61C3039:68..847			GTBX	CALc04805				2E-93			
24344	ENU08139	ANI61C1110 4:3777..2731			GTBX	AFUc12784				1.3E-86			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	% Description
24345	ENU08140	ANI61S2144: 274..16			GTBX	AFUc15701				6.1E-35			
24346	ENU08141	ANI61C1110 8:1698..2135			GTBX	AFUc09253				1.3E-29			
24347	ENU08142	ANI61C2315: 1253..672			GTBX	AFUc12154				1E-49			
24348	ENU08143	ANI61C2318: 473..1164			GTBX	AFUc07159				3.2E-63			
24349	ENU08144	ANI61C3049: 1395..2904			GTBX	FGRc02484				3.6E-39			
24350	ENU08145	ANI61S2150: 378..33			GTBX	AFUc02336				7.9E-61			
24351	ENU08146	ANI61C3050: 625..2162			GTBX	"AFUc12924, FGRc04111"				"9.5e-112, 1.7e-33"			
24352	ENU08147	ANI61C2321: 1194..529			GTBX	AFUc22220				7.8E-50			
24353	ENU08148	ANI61C3053: 2266..185			GTBX	"AFUc00609, AFUc14117, CALc02486"				"3.8e-21, 8.0e-195, 6.4e-24"			
24354	ENU08149	ANI61C3054: 747..2100			GTBX	"AFUc06449, AFUc07501, FGRc07589"				"1.6e-07, 9.4e-11, 1.5e-25"			
24355	ENU08150	ANI61C2325: 747..35			GTBX	AFUc13156				2.7E-24			
24356	ENU08151	ANI61C3057: 21..530			GTBX	Y13139				7.7e-28			
24357	ENU08152	ANI61C1112 0:693..4			GTBX	"AFUc01410, CALc06209"				"9.8e-76, 1.5e-39"			
24358	ENU08153	ANI61C1112 5:508..269			GTBX	CALc06229				9.5E-26			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr g	Description
24359	ENU08154	ANI61C1112 8:3194..4053			GTBX	"AFUc09503, CALc05722"				"1.9e-64, 2.7e-76"			
24360	ENU08155	ANI61S1437: 98..399			GTBX	"AFUc13604, AFUc15296"				"4.7e-25, 3.3e-21"			
24361	ENU08156	ANI61C2330: 2800..3374			GTBX	AFUc15919				1.1E-170			
24362	ENU08157	ANI61C2332: 4378..4578			GTBX	AFUc10180				2.8E-34			
24363	ENU08158	ANI61C3062: 2508..1335			GTBX	Y13134				5.7e-120			
24364	ENU08159	ANI61C1605: 643..1020			GTBX	AFUc10143				5.5E-28			
24365	ENU08160	ANI61C3064: 221..668			GTBX	AFUc13128				8.1E-56			
24366	ENU08161	ANI61C1606: 1693..539			GTBX	"AFUc16378, AFUc21308"				"1.1e-30, 9.5e-19"			
24367	ENU08162	ANI61C1607: 524..31			GTBX	AFUc06472				6.4E-37			
24368	ENU08163	ANI61C2338: 1791..877			GTBX	"AFUc07657, AFUc20776, FGRc03047"				"9.3e-58, 8.4e-27, 7.6e-15"			
24369	ENU08164	ANI61C1040 0:1011..199			GTBX	"AFUc15768, CALc05180"				"1.7e-65, 3.5e-30"			
24370	ENU08165	ANI61C1040 4:1681..456			GTBX	AFUc11156				1.7E-68			
24371	ENU08166	ANI61S2170: 458..150			GTBX	AFUc21244				5.8E-49			
24372	ENU08167	ANI61C2340: 1102..1321			GTBX	AFUc08035				2.2E-21			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24373	ENU08168	ANI61C3071: 303..1850			GTBX	AFUc06001				3.6E-49			
24374	ENU08169	ANI61C3071: 2656..2201			GTBX	AFUc11320				9.2E-37			
24375	ENU08170	ANI61C2342: 2..1100			GTBX	AFUc15644				3E-54			
24376	ENU08171	ANI61C2343: 385..998			GTBX	AFUc14858				1.2E-21			
24377	ENU08172	ANI61C1614: 1641..69			GTBX	"AFUc15021, FGRc09385"				"7.2e-79, 6.5e-61"			
24378	ENU08173	ANI61C2344: 772..1143			GTBX	AFUc15170				2.4E-32			
24379	ENU08174	ANI61C1616: 635..183			GTBX	AFUc13750				1.9E-41			
24380	ENU08175	ANI61C1618: 784..110			GTBX	AFUc10659				3.1E-61			
24381	ENU08176	ANI61C1619: 2385..1431			GTBX	"AFUc05005, AFUc10889, AFUc21670"				"2.2e-16, 2.4e-24, 2.0e-20"			
24382	ENU08177	ANI61C1041 2:1921..1718			GTBX	AFUc15311				2.9E-43			
24383	ENU08178	ANI61C1114 1:700..41			GTBX	AFUc09651				4.4E-31			
24384	ENU08179	ANI61C1041 5:1713..2470			GTBX	"AFUc08021, AFUc08021"				"1.5e-89, 2.0e-57"			
24385	ENU08180	ANI61C1041 6:448..26			GTBX	AFUc09679				3.7E-37			
24386	ENU08181	ANI61C1114 5:425..91			GTBX	CALc04731				4.5E-30			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24387	ENU08182	ANI61C1114 7:186..1347			GTBX	AFUc16242				1.8E-72			
24388	ENU08183	ANI61C3082: 496..1046			GTBX	AFUc05157				2.9E-38			
24389	ENU08184	ANI61C3085: 184..915			GTBX	"AFUc14050, AFUc20977"				"2.2e-50, 1.7e-18"			
24390	ENU08185	ANI61C3086: 61..600			GTBX	"AFUc21878, FGRc17423"				"3.0e-42, 2.4e-44"			
24391	ENU08186	ANI61C1042 0:3236..3461			GTBX	AFUc17331				9.8E-26			
24392	ENU08187	ANI61C1630: 739..967			GTBX	AFUc12693				2.2E-25			
24393	ENU08188	ANI61C3090: 4281..4003			GTBX	AFUc09749				8.6E-36			
24394	ENU08189	ANI61C1632: 3..711			GTBX	AFUc13580				4E-80			
24395	ENU08190	ANI61C1633: 895..350			GTBX	AFUc03062				2.2E-33			
24396	ENU08191	ANI61C3094: 77..861			GTBX	AFUc07151				1.3E-47			
24397	ENU08192	ANI61C1637: 500..782			GTBX	AFUc10559				5.6E-53			
24398	ENU08193	ANI61C2367: 2270..1947			GTBX	AFUc02537				7.4E-47			
24399	ENU08194	ANI61C2368: 1548..425			GTBX	AFUc15814				3.5E-57			
24400	ENU08195	ANI61C3097: 135..716			GTBX	"AFUc15533, AFUc15533"				"2.0e-70, 3.3e-35"			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr	% Description
24401	ENU08196	ANI61C2369: 3396..4360			GTBX	AFUc14374				2.3E-61			
24402	ENU08197	ANI61C1043 0:732..430			GTBX	"AFUc04312, AFUc04312"				"2.4e-38, 5.3e-50"			
24403	ENU08198	ANI61C1043 2:1380..543			GTBX	"AFUc09009, FGRc21606"				"9.8e-32, 5.5e-37"			
24404	ENU08199	ANI61C1116 3:615..1731			GTBX	Y13134				1.7e-84			
24405	ENU08200	ANI61C1116 7:1389..1628			GTBX	AFUc10437				8.1E-110			
24406	ENU08201	ANI61C1116 8:637..1234			GTBX	"AFUc05778, Y13139"				"9.9e-11, 4.5e-69"			
24407	ENU08202	ANI61C1646: 1677..1930			GTBX	AFUc14823				5.8E-91			
24408	ENU08203	ANI61C2376: 607..1538			GTBX	AFUc10283				2.4E-117			
24409	ENU08204	ANI61C1648: 1309..924			GTBX	AFUc15899				4.3E-26			
24410	ENU08205	ANI61C1117 2:3..540			GTBX	AFUc10300				2.3E-35			
24411	ENU08206	ANI61C1044 6:3962..6140			GTBX	"AFUc08784, AFUc20323, CALc05827, Y13136"				"3.0e-40, 4.1e-64, 1.3e-71, 2.4e-61"			
24412	ENU08207	ANI61C1117 7:38..1146			GTBX	"AFUc17428, AFUc22468"				"2.6e-29, 1.2e-69"			
24413	ENU08208	ANI61C1117 8:26..420			GTBX	FGRc03277				5.9E-21			
24414	ENU08209	ANI61C1654: 963..33			GTBX	CALc05018				1.1E-73			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24415	ENU08210	ANI61C2383: 772..341			GTBX	"AFUc13458, AFUc13458"				"1.4e-69, 6.6e-46"			
24416	ENU08211	ANI61C2386: 1473..1077			GTBX	AFUc05516				2.4E-35			
24417	ENU08212	ANI61C1657: 36..718			GTBX	AFUc01220				3.3E-30			
24418	ENU08213	ANI61C2387: 419..792			GTBX	"AFUc08391, U00093"				"1.1e-29, 1.5e-28"			
24419	ENU08214	ANI61C1045 2:2736..3671			GTBX	"AFUc01446, AFUc03449"				"3.6e-49, 5.3e-62"			
24420	ENU08215	ANI61C1045 5:10291..6040			GTBX	"AFUc02402, AFUc13896, AFUc15794, FGRC10936, FGRC19244"				"7.6e-13, 4.1e-90, 9.2e-59, 4.8e-08, 2.7e-24"			
24421	ENU08216	ANI61C1118 4:2930..1174			GTBX	"AFUc12122, AFUc19794"				"8.4e-30, 3.5e-11"			
24422	ENU08217	ANI61C1118 5:724..365			GTBX	AFUc17013				5.9E-43			
24423	ENU08218	ANI61C1118 6:6652..6341			GTBX	AFUc15274				7.9E-30			
24424	ENU08219	ANI61C1118 7:5255..6412			GTBX	AFUc11057				2.3E-165			
24425	ENU08220	ANI61C1118 8:3786..1817			GTBX	"AFUc03500, FGRC12085"				"3.9e-11, 1.6e-27"			
24426	ENU08221	ANI61C1118 9:437..772			GTBX	AFUc05827				2.1E-56			
24427	ENU08222	ANI61C2396: 4105..3424			GTBX	AFUc20773				1.9E-45			

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24428	ENU08223	ANI6IC1667:458..2025			GTBX	"AFUc01694, AFUc03534, AFUc09885"				"5.0e-13, 3.7e-37, 1.5e-68"			
24429	ENU08224	ANI6IC1046 0:2527..3230			GTBX	"AFUc10414, FGRc04734"				"3.0e-47, 4.3e-09"			
24430	ENU08225	ANI6IC1119 1:776..79			GTBX	AFUc15108				3.8E-31			
24431	ENU08226	ANI6IC1046 5:2467..4478			GTBX	"AFUc12339, AFUc12339"				"2.1e-67, 2.9e-31"			
24432	ENU08227	ANI6IC1046 8:4997..5533			GTBX	AFUc08587				8.5E-68			
24433	ENU08228	ANI6IC1119 9:60..490			GTBX	AFUc14731				1.9E-24			
24434	ENU08229	ANI6IC1672:893..597			GTBX	AFUc14113				6.4E-90			
24435	ENU08230	ANI6IC500:2 84..899			GTBX	AFUc12648				1.6E-30			
24436	ENU08231	ANI6IC504:7 20..1087			GTBX	FGRc12152				1.8E-64			
24437	ENU08232	ANI6IC508:3 282..3902			GTBX	AFUc04843				3.5E-38			
24438	ENU08233	ANI6IC1047 7:1761..819			GTBX	"FGRc06621, FGRc19870, FGRc21283"				"2.5e-17, 1.7e-14, 8.5e-50"			
24439	ENU08234	ANI6IC1683:611..1742			GTBX	"AFUc01385, AFUc06858, CALc02967"				"5.7e-25, 1.9e-46, 7.0e-43"			
24440	ENU08235	ANI6IC513:4 15..729			GTBX	FGRc09331				4.8E-67			
24441	ENU08236	ANI6IC1690:414..704			GTBX	AFUc04365				1.2E-36			

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24442	ENU08237	ANI61C524:1 24..354			GTBX	AFUc15671				8.4E-83			
24443	ENU08238	ANI61C525:7 223..2333			GTBX	"AFUc09623, AFUc15525, FGRc16821, Z12576, Y13138"				"1.0e-131, 8.9e-312, 4.1e-18, 0.0, 6.5e-82" "4.7e-64, 3.9e-188" 1.1E-65			
24444	ENU08239	ANI61C1049 0:5643..6771			GTBX	"AFUc05896, CALc06013"							
24445	ENU08240	ANI61C528:4 831..4175			GTBX	AFUc13014							
24446	ENU08241	ANI61C528:7 449..8035			GTBX	AFUc10735				1.8E-63			
24447	ENU08242	ANI61C1049 2:1047..2721			GTBX	"AFUc09485, AFUc15798"				"4.7e-32, 1.0e-98"			
24448	ENU08243	ANI61C1049 2:3842..4935			GTBX	"AFUc04378, AFUc07681"				"9.3e-63, 1.7e-11"			
24449	ENU08244	ANI61C529:4 2..431			GTBX	AFUc11443				2.3E-52			
24450	ENU08245	ANI61C1049 5:3717..6173			GTBX	"AFUc05971, AFUc11732, CALc05629, CALc05629"				"6.4e-92, 9.2e-131, 1.3e-193, 6.0e-37" 3.2E-56			
24451	ENU08246	ANI61C534:4 533..5332			GTBX	AFUc08068							
24452	ENU08247	ANI61C534:7 739..6453			GTBX	"AFUc19364, FGRc04608, FGRc14414"				"3.5e-33, 1.7e-10, 3.2e-25"			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrq	% Description
24453	ENU08248	ANI61C536:7 47..385			GTBX	AFUc09242				1.2E-32			
24454	ENU08249	ANI61C540:1 115..107			GTBX	"AFUc15779, FGRc15231, X59720"				"4.4e-109, 3.4e-42, 4.8e-08"			
24455	ENU08250	ANI61C543:5 4..1726			GTBX	"AFUc10780, CALc05902, Z71257"				"1.1e-30, 5.7e-131, 1.0e-59"			
24456	ENU08251	ANI61C8110: 2590..5977			GTBX	"AFUc15540, FGRc10976, FGRc25479"				"2.6e-137, 2.1e-79, 2.2e-11"			
24457	ENU08252	ANI61C8111: 1800..544			GTBX	AFUc11194				2E-70			
24458	ENU08253	ANI61C8113: 1223..2311			GTBX	CALc04732				2.2E-61			
24459	ENU08254	ANI61C8115: 2748..3329			GTBX	AFUc13681				6.9E-26			
24460	ENU08255	ANI61C8118: 2544..2122			GTBX	AFUc00564				4.7E-45			
24461	ENU08256	ANI61C556:1 452..2621			GTBX	AFUc08057				6.9E-42			
24462	ENU08257	ANI61C556:3 609..3139			GTBX	AFUc05897				8.2E-34			
24463	ENU08258	ANI61C8121: 828..109			GTBX	"AFUc11352, FGRc00210, Y13138"				"2.0e-55, 1.5e-25, 1.6e-29"			
24464	ENU08259	ANI61C8123: 2579..1657			GTBX	AFUc12416				2.2E-38			
24465	ENU08260	ANI61C8127: 1150..2			GTBX	"AFUc05079, AFUc05496"				"1.8e-26, 1.6e-23"			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	% Description
24466	ENU08261	ANI61C565:3 474..5173			GTBX	"Z71257				1.0e-107			
24467	ENU08262	ANI61C7402: 111..1536			GTBX	"AFUc06900, AFUc14568"				"2.3e-30, 5.9e-31"			
24468	ENU08263	ANI61C7406: 1092..374			GTBX	"AFUc04078, CALc05482"				"8.6e-47, 1.0e-69"			
24469	ENU08264	ANI61C8136: 3774..4745			GTBX	AFUc13396				2.2E-98			
24470	ENU08265	ANI61C8139: 4306..4841			GTBX	FGRc04774				3.1E-35			
24471	ENU08266	ANI61C576:4 55..90			GTBX	AFUc09285				5.9E-43			
24472	ENU08267	ANI61C8142: 2033..3024			GTBX	AFUc14097				3.3E-35			
24473	ENU08268	ANI61C7414: 299..789			GTBX	AFUc11487				4.3E-59			
24474	ENU08269	ANI61C8146: 340..23			GTBX	Y13138				1.6e-32			
24475	ENU08270	ANI61C8149: 1236..58			GTBX	AFUc15484				4.1E-88			
24476	ENU08271	ANI61C8154: 611..13			GTBX	AFUc01706				2.4E-23			
24477	ENU08272	ANI61C7427: 712..74			GTBX	Y13139				4.6e-19			
24478	ENU08273	ANI61C8158: 2634..1709			GTBX	AFUc12228				5.1E-25			
24479	ENU08274	ANI61C591:6 59..21			GTBX	AFUc10307				4.4E-69			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24480	ENU08275	ANI61C6703: 3206..4413			GTBX	"AFUc15895, FGRc12402"				"3.6e-40, 6.1e-31"			
24481	ENU08276	ANI61C6705: 4844..5990			GTBX	"AFUc13044, AFUc15912"				"2.2e-106, 3.6e-90"			
24482	ENU08277	ANI61C6710: 1220..1609			GTBX	AFUc01691				1.9E-27			
24483	ENU08278	ANI61C8171: 347..1607			GTBX	"AFUc08832, AFUc09980, FGRc01231"				"4.7e-50, 9.0e-34, 4.2e-51"			
24484	ENU08279	ANI61C8173: 440..2176			GTBX	"AFUc05587, AFUc07211, AFUc08234, AFUc21621"				"1.4e-107, 1.1e-65, 4.8e-95, 2.2e-46"			
24485	ENU08280	ANI61C6719: 484..128			GTBX	AFUc15031				1.6E-36			
24486	ENU08281	ANI61C6720: 349..919			GTBX	AFUc13243				2.8E-68			
24487	ENU08282	ANI61C7451: 1751..2032			GTBX	AFUc01939				1.1E-51			
24488	ENU08283	ANI61C8185: 431..1227			GTBX	"AFUc00988, CALc06038"				"3.3e-60, 2.8e-38"			
24489	ENU08284	ANI61C7457: 434..208			GTBX	AFUc15970				4.2E-78			
24490	ENU08285	ANI61C6728: 612..949			GTBX	AFUc08768				1.8E-44			
24491	ENU08286	ANI61C8188: 3201..1912			GTBX	"AFUc01114, AFUc18282, AFUc20635"				"1.3e-35, 1.4e-22, 8.8e-10"			
24492	ENU08287	ANI61C7459: 697..41			GTBX	AFUc04086				4E-82			

Genomic Organization

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24493	ENU08288	ANI61C6730: 156..509			GTBX	AFUc03916				1.4E-26			
24494	ENU08289	ANI61C8191: 1018..156			GTBX	AFUc09445				3.2E-100			
24495	ENU08290	ANI61C6734: 5607..6701			GTBX	"AFUc21317, Z71257"				"6.1e-07, 1.4e-32"			
24496	ENU08291	ANI61C7465: 1954..2550			GTBX	AFUc14734				3E-161			
24497	ENU08292	ANI61C8194: 2076..2470			GTBX	Y13137				8.2e-186			
24498	ENU08293	ANI61C6738: 5489..4467			GTBX	"AFUc01683, CALc04817, FGRC00806"				"1.6e-45, 3.1e-21, 1.6e-32"			
24499	ENU08294	ANI61C7475: 1427..483			GTBX	"AFUc17643, FGRC05979"				"1.2e-08, 1.2e-45"			
24500	ENU08295	ANI61C7476: 28..1165			GTBX	"AFUc02079, AFUc09659"				"3.0e-52, 7.5e-07"			
24501	ENU08296	ANI61C7479: 864..121			GTBX	AFUc04883				1.9E-88			
24502	ENU08297	ANI61C6750: 1592..800			GTBX	AFUc02986				4.9E-36			
24503	ENU08298	ANI61C7483: 5160..6015			GTBX	"AFUc12789, Y13134"				"3.0e-68, 1.5e-12"			
24504	ENU08299	ANI61C7486: 1350..379			GTBX	"AFUc02949, AFUc04582, FGRC10932"				"7.7e-71, 5.6e-39, 2.7e-18"			
24505	ENU08300	ANI61C6759: 2649..1266			GTBX	"AFUc10464, CALc06073"				"2.9e-71, 4.8e-98"			
24506	ENU08301	ANI61C7491: 481..1258			GTBX	AFUc15766				3.3E-67			

Genomic Coordinates

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	Description
24507	ENU08302	ANI61C6763: 845..1658			GTBX	"AFUc13390, AFUc13390"				"2.5e-45, 3.8e-77"			
24508	ENU08303	ANI61C7493: 1854..41			GTBX	AFUc15810				1.4E-236			
24509	ENU08304	ANI61C7499: 1893..2258			GTBX	AFUc09120				5.7E-46			
24510	ENU08305	ANI61C6771: 955..77			GTBX	"FGRc02670, Y13139"				"4.1e-40, 8.9e-18"			
24511	ENU08306	ANI61C6780: 1542..1913			GTBX	"AFUc17233, FGRc05382"				"7.2e-52, 1.2e-14"			
24512	ENU08307	ANI61C6782: 138..1073			GTBX	AFUc12300				9.2E-80			
24513	ENU08308	ANI61C6786: 269..868			GTBX	"AFUc03905, CALc03405"				"6.3e-25, 3.1e-20"			
24514	ENU08309	ANI61C6789: 1667..164			GTBX	AFUc12649				3E-156			
24515	ENU08310	ANI61S448:4 50..153			GTBX	FGRc24169				2.3E-21			
24516	ENU08311	ANI61C6792: 700..1644			GTBX	"AFUc06967, FGRc12581"				"7.2e-93, 6.8e-27"			
24517	ENU08312	ANI61C6797: 1035..50			GTBX	Y13135				1.3e-48			
24518	ENU08313	ANI61S2206: 326..28			GTBX	AFUc12261				2E-33			
24519	ENU08314	ANI61C3111: 393..719			GTBX	AFUc15581				2.3E-67			
24520	ENU08315	ANI61C3114: 2..476			GTBX	AFUc10952				1E-22			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24521	ENU08316	ANI61C3120: 317..649			GTBX	AFUc14123				8.4E-42			
24522	ENU08317	ANI61C3122: 3..329			GTBX	"AFUc15397, AFUc15397"				"2.9e-45, 3.3e-72"			
24523	ENU08318	ANI61C3133: 776..1003			GTBX	AI001370				6.5e-14			
24524	ENU08319	ANI61C2406: 34..768			GTBX	"AFUc10109, FGRe24183"				"7.3e-07, 5.1e-25"			
24525	ENU08320	ANI61C3138: 1800..2489			GTBX	AFUc09498				1.4E-33			
24526	ENU08321	ANI61C2409: 23..820			GTBX	AFUc10750				2E-71			
24527	ENU08322	ANI61C1120 5:842..1238			GTBX	AFUc21643				1.3E-32			
24528	ENU08323	ANI61C1120 5:7773..7272			GTBX	AFUc06894				6.5E-33			
24529	ENU08324	ANI61C1120 5:10041..10386			GTBX	Z71256				1.6e-24			
24530	ENU08325	ANI61C1120 5:11046..11351			GTBX	AFUc12485				6.5E-33			
24531	ENU08326	ANI61S1516: 546..243			GTBX	AFUc01209				3.3E-46			
24532	ENU08327	ANI61C2411: 175..744			GTBX	"AFUc06238, AFUc21228"				"1.6e-65, 6.8e-08"			
24533	ENU08328	ANI61C2411: 2361..1216			GTBX	"AFUc03672, CALc04359, Y13139"				"1.9e-38, 1.1e-41, 1.9e-46"			
24534	ENU08329	ANI61C3145: 4077..2208			GTBX	"AFUc03167, AFUc13827"				"9.6e-59, 1.2e-88"			

66666" Description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24535	ENU08330	ANI61C3148: 230..1073			GTBX	CALc04288				1.6E-87			
24536	ENU08331	ANI61C1121 0:954..656			GTBX	AFUc14655				3.6E-46			
24537	ENU08332	ANI61C1121 1:1639..690			GTBX	"AFUc05869, AFUc10580, CALc05396"				"1.3e-83, 6.3e-32, 2.3e-89"			
24538	ENU08333	ANI61C1121 4:784..401			GTBX	AFUc15114				1.7E-60			
24539	ENU08334	ANI61C1121 5:541..134			GTBX	AFUc16004				3.7E-24			
24540	ENU08335	ANI61C2420: 2226..2459			GTBX	AFUc03940				6.5E-27			
24541	ENU08336	ANI61C2421: 1057..1414			GTBX	AFUc14756				6.7E-28			
24542	ENU08337	ANI61C2422: 257..1093			GTBX	"AFUc03549, AFUc13726, AFUc13726"				"5.5e-44, 1.6e-28, 2.0e-32"			
24543	ENU08338	ANI61C3152: 439..3434			GTBX	"AFUc11188, U00093"				"1.5e-114, 4.5e-202"			
24544	ENU08339	ANI61C3157: 40..494			GTBX	AFUc21873				2.7E-28			
24545	ENU08340	ANI61C3158: 3582..2955			GTBX	AFUc07435				1.2E-47			
24546	ENU08341	ANI61C1122 3:2614..2006			GTBX	CALc05628				2.8E-47			
24547	ENU08342	ANI61C1122 9:5179..6489			GTBX	"AFUc11755, Y13135"				"2.0e-63, 5.7e-100"			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24548	ENU08343	ANI61C2431: 976..59			GTBX	"AFUc01570, AFUc08276"				"4.3e-28, 4.5e-32"			
24549	ENU08344	ANI61C1705: 4995..6299			GTBX	"AFUc00996, Y13134"				"2.1e-19, 9.6e-50"			
24550	ENU08345	ANI61C3165: 211..726			GTBX	CALc05020				4.8E-24			
24551	ENU08346	ANI61C3166: 752..138			GTBX	AFUc13944				2.1E-53			
24552	ENU08347	ANI61C2437: 2200..3538			GTBX	"AFUc01000, AFUc04109, FGRc04331"				"1.2e-28, 2.5e-53, 1.1e-51"			
24553	ENU08348	ANI61C1123 0:3214..1952			GTBX	"AFUc14997, AFUc14997"				"6.3e-80, 6.5e-66"			
24554	ENU08349	ANI61C1050 1:6263..7127			GTBX	Y13138				0.0			
24555	ENU08350	ANI61C1050 6:2..538			GTBX	CALc06073				3.1E-47			
24556	ENU08351	ANI61C1050 8:522..79			GTBX	AFUc13411				3.9E-26			
24557	ENU08352	ANI61C3170: 1199..657			GTBX	AFUc14288				1.1E-73			
24558	ENU08353	ANI61C1713: 2645..1891			GTBX	AFUc03044				4.3E-26			
24559	ENU08354	ANI61C2446: 844..49			GTBX	"AFUc12955, AFUc12955"				"4.9e-32, 9.8e-62"			
24560	ENU08355	ANI61C3177: 3..1536			GTBX	AFUc14427				6.3E-206			
24561	ENU08356	ANI61C2449: 872..402			GTBX	AFUc08082				2.2E-37			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24562	ENU08357	ANI61C1051 0:802..64			GTBX	"AFUc07339, CALc05205"				"1.5e-12, 3.1e-65"			
24563	ENU08358	ANI61C1124 4:331..774			GTBX	FGRc11233				3.4E-30			
24564	ENU08359	ANI61C1124 7:390..923			GTBX	"AFUc18726, AFUc19650"				"1.9e-34, 3.1e-43"			
24565	ENU08360	ANI61C1124 8:23..337			GTBX	AFUc11164				8.1E-22			
24566	ENU08361	ANI61C1720: 1126..146			GTBX	CALc06237				1.6E-27			
24567	ENU08362	ANI61C2450: 1275..88			GTBX	"AFUc09645, FGRc11399, Z4707"				"4.6e-38, 1.9e-11, 2.9e-26"			
24568	ENU08363	ANI61C2455: 1089..1600			GTBX	AFUc06803				4.7E-46			
24569	ENU08364	ANI61C1726: 3193..2059			GTBX	AFUc12449				6.8E-58			
24570	ENU08365	ANI61C3187: 2309..2737			GTBX	AFUc10771				1.6E-42			
24571	ENU08366	ANI61C2459: 3630..4313			GTBX	AFUc04986				8.6E-77			
24572	ENU08367	ANI61C1052 6:98..790			GTBX	"AFUc03097, AFUc07509"				"5.2e-13, 2.5e-67"			
24573	ENU08368	ANI61C1125 7:320..47			GTBX	AFUc08915				7.9E-28			
24574	ENU08369	ANI61C1052 8:381..724			GTBX	AFUc04981				3E-23			
24575	ENU08370	ANI61C1052 9:1858..763			GTBX	AFUc01784				2.8E-27			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24576	ENU08371	ANI61C2461: 2065..212			GTBX	AFUc10369				8.3E-53			
24577	ENU08372	ANI61C2465: 698..3702			GTBX	"AFUc07667, AFUc12566, AFUc13531, AFUc14327, AFUc14338, AFUc15132, FGRc00835, FGRc17112"				"4.3e-12, 1.1e-38, 3.3e-23, 2.0e-42, 2.0e-63, 2.5e-52, 6.0e-27, 1.2e-08"			
24578	ENU08373	ANI61C3199: 1590..2454			GTBX	"AFUc05935, AFUc15519"				"1.3e-10, 1.3e-45"			
24579	ENU08374	ANI61C1126 0:326..605			GTBX	"AFUc15094, AFUc15094, Y13134"				"2.3e-14, 4.6e-17, 2.0e-24"			
24580	ENU08375	ANI61C1126 3:305..27			GTBX	AFUc09950				3.4E-34			
24581	ENU08376	ANI61C1053 4:344..592			GTBX	AFUc13512				2.2E-56			
24582	ENU08377	ANI61C1053 5:4543..3779			GTBX	AFUc14535				1.7E-97			
24583	ENU08378	ANI61C1126 4:350..51			GTBX	AFUc09251				2.3E-41			
24584	ENU08379	ANI61C1126 8:188..526			GTBX	AFUc09884				2.5E-21			
24585	ENU08380	ANI61C1743: 412..1446			GTBX	"AFUc07667, AFUc08168, AFUc08900, AFUc14327"				"3.8e-15, 7.4e-50, 4.1e-11, 5.1e-48"			
24586	ENU08381	ANI61C2475: 1147..548			GTBX	AFUc02096				1.4E-43			
24587	ENU08382	ANI61C2479: 1298..1026			GTBX	AFUc06657				1.2E-22			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24601	ENU08396	ANI61C1765: 3849..4804			GTBX	AFUc08160				2.4E-108			
24602	ENU08397	ANI61C1768: 1071..245			GTBX	"CALc05020, FGRc07538, Y13134"				"2.8e-133, 2.6e-107, 2.6e-107"			
24603	ENU08398	ANI61C1769: 630..424			GTBX	AFUc15659				1.1E-24			
24604	ENU08399	ANI61C1056 0:379..587			GTBX	FGRc10510				1.5E-36			
24605	ENU08400	ANI61C1129 1:680..3			GTBX	"AFUc01382, AFUc06747"				"2.4e-16, 2.3e-108"			
24606	ENU08401	ANI61C1129 2:992..1827			GTBX	"AFUc01815, AFUc19145"				"4.1e-10, 5.5e-40"			
24607	ENU08402	ANI61C1129 3:1130..708			GTBX	"AFUc09000, Y13134"				"3.5e-81, 4.3e-40"			
24608	ENU08403	ANI61C1129 4:28..565			GTBX	AFUc04474				6E-68			
24609	ENU08404	ANI61C1129 8:975..145			GTBX	"CALc04432, FGRc05226"				"8.9e-80, 2.7e-19"			
24610	ENU08405	ANI61C1129 9:1350..1568			GTBX	CALc03902				7E-40			
24611	ENU08406	ANI61C1774: 450..851			GTBX	AFUc11966				5.9E-46			
24612	ENU08407	ANI61C1779: 391..849			GTBX	AFUc12781				9.6E-30			
24613	ENU08408	ANI61C1057 4:957..691			GTBX	AFUc09666				2.4E-38			

Gene Description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24614	ENU08409	ANI61C1781:5..532			GTBX	"AFUc09001, CALc06053"				"3.6e-17, 7.5e-30"			
24615	ENU08410	ANI61C614:8 1..879			GTBX	AFUc21798				8.5E-31			
24616	ENU08411	ANI61C617:7 90..344			GTBX	AFUc01603				8.4E-73			
24617	ENU08412	ANI61C1058 7:125..1577			GTBX	"AFUc13537, AFUc15937, AFUc16854, AFUc18057"				"6.1e-43, 9.1e-33, 5.3e-07, 7.5e-60"			
24618	ENU08413	ANI61C1058 9:4717..6120			GTBX	AFUc16933				8.6E-28			
24619	ENU08414	ANI61C621:9 88..27			GTBX	AFUc13969				3.8E-62			
24620	ENU08415	ANI61C629:1 426..1674			GTBX	AFUc10182				2.2E-44			
24621	ENU08416	ANI61C632:2 615..2967			GTBX	AFUc13337				2.6E-69			
24622	ENU08417	ANI61C638:1 513..642			GTBX	AFUc13559				1.7E-119			
24623	ENU08418	ANI61C8202:2327..2693			GTBX	AFUc09447				1.7E-72			
24624	ENU08419	ANI61C8205:1..564			GTBX	AFUc11001				1.7E-28			
24625	ENU08420	ANI61C8211:438..914			GTBX	AFUc10534				3.7E-117			
24626	ENU08421	ANI61C8212:1480..1118			GTBX	AFUc15391				3.5E-112			
24627	ENU08422	ANI61C8220:4..444			GTBX	AFUc05936				2.8E-55			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24628	ENU08423	ANI61C8225:1437..173			GTBX	"AFUc05414, CALc04219"				"7.7e-59, 4.0e-44"			
24629	ENU08424	ANI61C661:391..8			GTBX	AFUc07993				4.6E-33			
24630	ENU08425	ANI61C7502:2085..4478			GTBX	"AFUc11007, Y13135"				"2.0e-65, 1.3e-154"			
24631	ENU08426	ANI61C7503:2046..2255			GTBX	Y13134				3.1e-237			
24632	ENU08427	ANI61C8233:608..326			GTBX	"AFUc15337, AFUc15337"				"3.3e-113, 4.3e-123"			
24633	ENU08428	ANI61C8235:1473..2074			GTBX	"AFUc12073, CALc06007"				"3.1e-32, 1.9e-83"			
24634	ENU08429	ANI61C8236:542..1400			GTBX	AFUc00714				6.8E-52			
24635	ENU08430	ANI61C8238:950..1813			GTBX	AFUc20930				2.6E-32			
24636	ENU08431	ANI61C670:364..585			GTBX	AFUc13626				6.8E-35			
24637	ENU08432	ANI61C671:112..549			GTBX	"AFUc15558, AFUc15558"				"2.0e-65, 4.8e-61"			
24638	ENU08433	ANI61C678:814..30			GTBX	AFUc13964				1.5E-29			
24639	ENU08434	ANI61C8245:1570..437			GTBX	"AFUc14341, FGRC04315"				"1.6e-105, 5.4e-36"			
24640	ENU08435	ANI61C682:2213..1222			GTBX	AFUc15961				1.5E-25			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24654	ENU08449	ANI61C8269: 46..569			GTBX	AFUc07452				1.1E-34			
24655	ENU08450	ANI61C6810: 5679..6098			GTBX	AFUc19773				1.5E-29			
24656	ENU08451	ANI61C8270: 427..31			GTBX	"AFUc04808, AFUc04808"				"2.1e-45, 7.2e-47"			
24657	ENU08452	ANI61C8271: 986..34			GTBX	AFUc15466				1.5E-46			
24658	ENU08453	ANI61C7542: 122..989			GTBX	"AFUc11101, AFUc11101"				"4.8e-38, 8.3e-26"			
24659	ENU08454	ANI61C7543: 1033..176			GTBX	"AFUc15495, FGRC16134"				"8.0e-47, 4.6e-07"			
24660	ENU08455	ANI61C8272: 1151..1600			GTBX	AFUc14280				1.7E-82			
24661	ENU08456	ANI61C6815: 1176..454			GTBX	FGRC10208				5.2E-54			
24662	ENU08457	ANI61C7549: 1848..425			GTBX	"AFUc04568, FGRC00446"				"2.7e-28, 8.6e-14"			
24663	ENU08458	ANI61C8279: 1068..691			GTBX	FGRC20509				1.3E-23			
24664	ENU08459	ANI61C6820: 1111..501			GTBX	AFUc03505				1.6E-49			
24665	ENU08460	ANI61C8286: 479..137			GTBX	AFUc15334				1.6E-21			
24666	ENU08461	ANI61C8286: 839..1285			GTBX	AFUc14069				9.5E-45			
24667	ENU08462	ANI61C6829: 1840..166			GTBX	"CALc03297, Y13139"				"1.2e-17, 3.4e-56"			

Gene description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24668	ENU08463	ANI61C8288: 1325..501			GTBX	AFUc05810				2.6E-31			
24669	ENU08464	ANI61C6831: 148..1585			GTBX	"AFUc04998, FGRc01824"				"5.7e-56, 3.5e-16"			
24670	ENU08465	ANI61C6834: 357..867			GTBX	"AFUc12667, AFUc15842"				"8.8e-56, 2.3e-15"			
24671	ENU08466	ANI61C7563: 1403..972			GTBX	AFUc06136				1.6E-52			
24672	ENU08467	ANI61C6835: 679..1407			GTBX	AFUc03378				6.6E-21			
24673	ENU08468	ANI61C8295: 336..1098			GTBX	"FGRc00692, FGRc11948"				"3.8e-30, 3.3e-22"			
24674	ENU08469	ANI61C7566: 1430..741			GTBX	AFUc19723				3.7E-27			
24675	ENU08470	ANI61C6839: 5869..5612			GTBX	"AFUc04055, AFUc05745"				"3.1e-13, 8.0e-61"			
24676	ENU08471	ANI61C8299: 716..3012			GTBX	"AFUc09176, AFUc09176, FGRc09522"				"1.3e-165, 2.6e-63, 7.0e-09"			
24677	ENU08472	ANI61C7570: 583..1210			GTBX	FGRc00007				2.2E-68			
24678	ENU08473	ANI61C7571: 608..210			GTBX	AFUc10686				1E-25			
24679	ENU08474	ANI61C7577: 78..566			GTBX	AFUc00513				8.2E-23			
24680	ENU08475	ANI61C7578: 2539..2834			GTBX	AFUc02252				3.3E-31			
24681	ENU08476	ANI61C7587: 2348..2067			GTBX	FGRc12388				3E-31			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24682	ENU08477	ANI61C7588:1381..602			GTBX	"AFUc06763, AFUc07411, FGRc21800"				"2.5e-71, 1.4e-13, 2.1e-20"			
24683	ENU08478	ANI61S519:2..592			GTBX	"FGRc07962, FGRc16898"				"1.1e-09, 1.8e-29"			
24684	ENU08479	ANI61C7591:1015..1599			GTBX	AFUc12136				2.1E-78			
24685	ENU08480	ANI61C6863:1573..1244			GTBX	AFUc10542				7.8E-26			
24686	ENU08481	ANI61C6864:2992..4626			GTBX	"AFUc07814, CALc01848, Z17256"				"2.5e-77, 6.1e-27, 2.2e-30"			
24687	ENU08482	ANI61C6870:949..73			GTBX	"AFUc09260, CALc05985"				"1.4e-91, 4.6e-57"			
24688	ENU08483	ANI61C6874:509..30			GTBX	AFUc15201				8.3E-117			
24689	ENU08484	ANI61C6875:478..1035			GTBX	"AFUc15186, AFUc15186"				"2.1e-45, 9.8e-52"			
24690	ENU08485	ANI61C6883:6..281			GTBX	AFUc08480				2.3E-27			
24691	ENU08486	ANI61C6883:1538..1254			GTBX	AFUc08221				6.7E-38			
24692	ENU08487	ANI61C6888:2405..2970			GTBX	AFUc11742				1.8E-66			
24693	ENU08488	ANI61C6890:1004..189			GTBX	AFUc08698				4E-54			
24694	ENU08489	ANI61C6890:1898..2209			GTBX	AFUc09533				2.4E-56			
24695	ENU08490	ANI61C6891:1691..1221			GTBX	AFUc03109				5.6E-25			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24696	ENU08491	ANI61C6896: 960..191			GTBX	AFUc14439				6.5E-64			
24697	ENU08492	ANI61C6897: 9..776			GTBX	AFUc12120				2E-37			
24698	ENU08493	ANI61S2306: 399..4			GTBX	"AFUc13642, Y13138"				"4.5e-52, 4.1e-09"			
24699	ENU08494	ANI61C3208: 1447..1953			GTBX	AFUc10936				5.8E-66			
24700	ENU08495	ANI61C3209: 956..2284			GTBX	AFUc15271				8.2E-44			
24701	ENU08496	ANI61S2314: 70..548			GTBX	CALc06228				2.1E-21			
24702	ENU08497	ANI61S3044: 78..524			GTBX	CALc05604				6E-28			
24703	ENU08498	ANI61C3211: 1102..2301			GTBX	"AFUc19019, FGRc18454, Y13138"				"1.4e-48, 1.4e-29, 5.3e-105"			
24704	ENU08499	ANI61C3214: 567..1777			GTBX	"AFUc19711, AFUc21339"				"8.6e-54, 5.8e-35"			
24705	ENU08500	ANI61C3215: 3946..5307			GTBX	"AFUc12382, AFUc15610"				"2.2e-89, 6.9e-46"			
24706	ENU08501	ANI61C3217: 1504..2206			GTBX	"AFUc13189, AFUc21901"				"9.0e-158, 9.1e-10"			
24707	ENU08502	ANI61S2328: 554..315			GTBX	"AFUc10225, Z71257"				"1.5e-14, 7.1e-55"			
24708	ENU08503	ANI61C3226: 785..93			GTBX	"AFUc08295, AFUc08295"				"1.9e-41, 7.2e-37"			
24709	ENU08504	ANI61C2503: 1119..1520			GTBX	"FGRc05378, FGRc11560"				"8.0e-32, 7.5e-31"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24710	ENU08505	ANI61C3235: 59..1675			GTBX	"AFUc01811, AFUc13887, CALc04895, FGRc00754, FGRc05142"				"1.3e-75, 1.1e-16, 3.0e-61, 1.2e-51, 2.5e-23" 4.8E-29			
24711	ENU08506	ANI61C3236: 1660..614			GTBX	AFUc10571							
24712	ENU08507	ANI61C2507: 1225..200			GTBX	"AFUc02726, AFUc04017"				"1.0e-27, 3.9e-66"			
24713	ENU08508	ANI61C2508: 906..65			GTBX	AFUc04584				3.6E-41			
24714	ENU08509	ANI61C2509: 1495..683			GTBX	AFUc14282				1.2E-102			
24715	ENU08510	ANI61C3238: 2274..3441			GTBX	CALc05093				5E-33			
24716	ENU08511	ANI61C1130 0:1611..872			GTBX	Z71257				2.2e-76			
24717	ENU08512	ANI61C1130 1:137..2796			GTBX	"AFUc05446, AFUc08551, AFUc16108, AFUc20988, CALc01643"				"7.2e-11, 2.8e-38, 3.1e-61, 2.3e-43, 1.5e-17" 3.6E-63			
24718	ENU08513	ANI61C2510: 555..49			GTBX	CALc05636							
24719	ENU08514	ANI61C2511: 1515..260			GTBX	CALc05278				6.4E-124			
24720	ENU08515	ANI61C2512: 41..685			GTBX	AFUc14444				3.6E-48			
24721	ENU08516	ANI61C3245: 2214..196			GTBX	"AFUc15224, FGRc07913"				"4.4e-65, 7.4e-51"			
24722	ENU08517	ANI61C1131 7:109..887			GTBX	AFUc06140				1.4E-48			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24723	ENU08518	ANI61S3085:1..474			GTBX	AFUc10385				6E-34			
24724	ENU08519	ANI61C3251:2782..3157			GTBX	AFUc13043				4.6E-49			
24725	ENU08520	ANI61C3255:2764..2980			GTBX	Y13140				9.5e-39			
24726	ENU08521	ANI61C11325:653..41			GTBX	AFUc10893				2.6E-39			
24727	ENU08522	ANI61C11328:1793..19			GTBX	"AFUc02484, AFUc04329, AFUc14153"				"2.1e-21, 2.0e-53, 2.9e-174"			
24728	ENU08523	ANI61C3261:2760..3156			GTBX	AFUc15767				1.4E-271			
24729	ENU08524	ANI61C3262:516..42			GTBX	AFUc16517				6.2E-38			
24730	ENU08525	ANI61C3264:1738..2478			GTBX	"AFUc02688, AFUc15728, AFUc15728"				"1.7e-46, 2.2e-30, 6.4e-109"			
24731	ENU08526	ANI61C2538:16..453			GTBX	"AFUc14903, AFUc15880"				"9.3e-25, 8.8e-07"			
24732	ENU08527	ANI61C10601:1012..2306			GTBX	"CALc06147, FGRc12101"				"2.7e-25, 6.2e-23"			
24733	ENU08528	ANI61C10602:1474..542			GTBX	"AFUc03068, FGRc11923"				"1.3e-91, 7.4e-43"			
24734	ENU08529	ANI61C11332:469..3			GTBX	FGRc25342				8.3E-21			
24735	ENU08530	ANI61C11333:419..3			GTBX	AFUc07909				4.1E-39			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24763	ENU08558	ANI61C2568: 24..638			GTBX	AFUc05821				1.1E-28			
24764	ENU08559	ANI61C1839: 330..1127			GTBX	"AFUc09025, AFUc11515"				"6.1e-41, 5.2e-77"			
24765	ENU08560	ANI61C1063 0:465..32			GTBX	AFUc05997				6.4E-30			
24766	ENU08561	ANI61C1063 1:186..1843			GTBX	"AFUc01713, AFUc05435, AFUc05435"				"1.3e-63, 6.4e-41, 6.5e-55"			
24767	ENU08562	ANI61C1840: 1346..639			GTBX	AFUc18505				1.1E-37			
24768	ENU08563	ANI61C1843: 115..501			GTBX	FGRc11281				8.9E-46			
24769	ENU08564	ANI61C1846: 284..1741			GTBX	"FGRc02282, FGRc05940, FGRc11631"				"2.6e-23, 1.4e-13, 1.3e-09"			
24770	ENU08565	ANI61C2577: 199..920			GTBX	"CALc05069, FGRc17612"				"2.7e-41, 6.0e-44"			
24771	ENU08566	ANI61C1064 1:1707..3655			GTBX	"AFUc11683, Y13135"				"3.3e-190, 5.1e-119"			
24772	ENU08567	ANI61C1137 2:74..894			GTBX	AFUc17844				3.7E-26			
24773	ENU08568	ANI61C1064 5:47..619			GTBX	AFUc21723				2E-68			
24774	ENU08569	ANI61C2582: 5424..5048			GTBX	AFUc01594				1.5E-28			
24775	ENU08570	ANI61C1856: 658..141			GTBX	AFUc16536				3.5E-26			
24776	ENU08571	ANI61C2588: 754..22			GTBX	"AFUc08407, FGRc10457"				"4.6e-49, 6.6e-60"			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrq %	Description
24777	ENU08572	ANI61C2589:186..1330			GTBX	AFUc13209				8.9E-77			
24778	ENU08573	ANI61C11381:1081..1457			GTBX	AFUc17037				5.9E-32			
24779	ENU08574	ANI61C11383:624..383			GTBX	FGRc08856				4.6E-27			
24780	ENU08575	ANI61C10654:7892..8920			GTBX	Y13135				3.8e-149			
24781	ENU08576	ANI61C10655:912..54			GTBX	CALc06050				4.2E-84			
24782	ENU08577	ANI61C10657:6666..6094			GTBX	AFUc03173				6.6E-39			
24783	ENU08578	ANI61C11388:62..701			GTBX	AFUc15731				4.1E-47			
24784	ENU08579	ANI61C1861:1870..524			GTBX	AFUc14963				3E-180			
24785	ENU08580	ANI61C2592:1363..3			GTBX	"AFUc17647, FGRc25036"				"9.1e-29, 1.8e-53"			
24786	ENU08581	ANI61C1865:1589..2224			GTBX	AFUc06633				1.4E-63			
24787	ENU08582	ANI61C2594:5002..1392			GTBX	"AFUc09935, Y13140"				"3.6e-55, 0.0"			
24788	ENU08583	ANI61C1866:1568..1080			GTBX	AFUc10713				4.1E-44			
24789	ENU08584	ANI61C2599:460..72			GTBX	Y13135				2.6e-62			
24790	ENU08585	ANI61C10665:664..406			GTBX	AFUc02315				5.3E-23			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24791	ENU08586	ANI61C1139 5:3021..2575			GTBX	AFUc22562				1.1E-28			
24792	ENU08587	ANI61C1871: 260..54			GTBX	"AFUc01385, AFUc09613"				"3.1e-34, 1.1e-19"			
24793	ENU08588	ANI61C1067 3:922..1413			GTBX	CALc03969				3.2E-57			
24794	ENU08589	ANI61C1067 5:2719..1441			GTBX	"AFUc15461, AFUc15461"				"1.2e-96, 2.3e-121"			
24795	ENU08590	ANI61C1067 5:3404..3889			GTBX	AFUc10889				2.7E-50			
24796	ENU08591	ANI61C1067 8:1080..600			GTBX	AFUc11094				8.3E-27			
24797	ENU08592	ANI61C9002: 1846..878			GTBX	AFUc11192				3.2E-94			
24798	ENU08593	ANI61C9004: 3235..3965			GTBX	"AFUc11110, Y13138"				"5.7e-30, 1.2e-14"			
24799	ENU08594	ANI61C9008: 314..861			GTBX	AFUc12481				2.4E-63			
24800	ENU08595	ANI61C1880: 72..1179			GTBX	"AFUc04431, AFUc16451"				"1.6e-82, 2.8e-14"			
24801	ENU08596	ANI61C1883: 546..19			GTBX	AFUc21307				3.5E-30			
24802	ENU08597	ANI61C1885: 1021..95			GTBX	AFUc10552				1.1E-64			
24803	ENU08598	ANI61C710:2 805..1017			GTBX	"AFUc11549, AFUc15367, AFUc17813"				"1.5e-81, 1.0e-41, 4.1e-53"			
24804	ENU08599	ANI61C713:1 670..74			GTBX	"AFUc05242, AFUc10990"				"6.0e-55, 2.5e-114"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24805	ENU08600	ANI61C1068 3:1487..1242			GTBX	AFUc13939				1.4E-22			
24806	ENU08601	ANI61C1068 9:1065..390			GTBX	"AFUc13250, FGRc13107"				"6.4e-93, 1.4e-10"			
24807	ENU08602	ANI61C9015: 405..1			GTBX	AFUc12921				3.1E-56			
24808	ENU08603	ANI61C1895: 23..652			GTBX	AFUc10988				1.4E-60			
24809	ENU08604	ANI61C720:1 602..685			GTBX	CALc06106				3.6E-78			
24810	ENU08605	ANI61C1069 5:865..252			GTBX	AFUc10487				9.9E-50			
24811	ENU08606	ANI61C9025: 463..194			GTBX	AFUc00949				5.1E-49			
24812	ENU08607	ANI61C8300: 800..189			GTBX	"AFUc08390, AFUc13837"				"3.3e-41, 6.5e-22"			
24813	ENU08608	ANI61C9030: 1085..11			GTBX	"AFUc06221, CALc06213, Y13134"				"8.3e-40, 2.3e-13, 4.6e-13"			
24814	ENU08609	ANI61C9039: 5769..6530			GTBX	"AFUc00570, FGRc14945"				"3.4e-28, 2.5e-08"			
24815	ENU08610	ANI61C8310: 465..181			GTBX	FGRc10180				3.2E-24			
24816	ENU08611	ANI61C8314: 2724..2023			GTBX	AFUc21917				5.4E-31			
24817	ENU08612	ANI61C9048: 61..1497			GTBX	"AFUc14050, FGRc03000"				"1.3e-98, 3.4e-28"			
24818	ENU08613	ANI61C751:4 20..749			GTBX	AFUc06278				1.4E-42			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24819	ENU08614	ANI61C758:4 029..103			GTBX	"AFUc05783, AFUc05961, AFUc12204, AFUc12677, CALc06075, FGRc11436, FGRc17690"				"2.5e-72, 1.5e-27, 6.6e- 196, 7.1e- 126, 8.6e- 128, 3.7e-75, 2.9e-35" "5.8e-26, 1.3e-23"			
24820	ENU08615	ANI61C8322: 1663..1077			GTBX	"AFUc04172, FGRc02654"				3.5E-37			
24821	ENU08616	ANI61C8325: 79..477			GTBX	AFUc12859							
24822	ENU08617	ANI61C8326: 860..1122			GTBX	AFUc09750				1.8E-25			
24823	ENU08618	ANI61C8330: 1999..807			GTBX	"AFUc02770, AFUc09905"				"8.7e-69, 1.6e-54"			
24824	ENU08619	ANI61C7605: 1939..1517			GTBX	AFUc09154				4.4E-30			
24825	ENU08620	ANI61C9063: 6060..4119			GTBX	"AFUc13510, AFUc14636, FGRc04398"				"1.4e-81, 1.8e- 100, 1.1e-08" 1.7E-35			
24826	ENU08621	ANI61C7606: 185..886			GTBX	AFUc09586							
24827	ENU08622	ANI61C9067: 4043..1889			GTBX	"AFUc09078, AFUc18318, FGRc07495, FGRc07643"				"1.5e-11, 4.3e-09, 6.4e-29, 1.4e-29" 1.1E-58			
24828	ENU08623	ANI61C770:7 83..35			GTBX	AFUc01959							
24829	ENU08624	ANI61C775:4 81..1025			GTBX	"AFUc04122, Y13139"				"7.8e-21, 5.9e-61"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24830	ENU08625	ANI61C8340: 600..1358			GTBX	"AFUc09848, FGRc00517"				"2.6e-41, 1.0e-27"			
24831	ENU08626	ANI61C7615: 53..558			GTBX	AFUc01625				3.5E-52			
24832	ENU08627	ANI61C7616: 3166..2391			GTBX	"AFUc00961, FGRc05631"				"1.7e-25, 5.5e-16"			
24833	ENU08628	ANI61C7617: 1020..82			GTBX	"AFUc13516, CALc04464"				"1.8e-84, 9.5e-47"			
24834	ENU08629	ANI61C7618: 449..192			GTBX	AFUc12936				6.3E-53			
24835	ENU08630	ANI61C9077: 618..241			GTBX	AFUc02355				2.6E-33			
24836	ENU08631	ANI61C8348: 1562..2188			GTBX	AFUc06232				1.9E-58			
24837	ENU08632	ANI61C9078: 2867..1238			GTBX	"CALc05373, FGRc09215, FGRc14791, Y13140"				"1.3e-93, 1.3e-21, 1.1e-43, 9.9e-187"			
24838	ENU08633	ANI61C780:4 46..1			GTBX	"AFUc13983, Y13137"				"2.6e-42, 4.3e-33"			
24839	ENU08634	ANI61C781:6 3..979			GTBX	AFUc10848				5.4E-43			
24840	ENU08635	ANI61C789:4 022..2710			GTBX	"AFUc16570, AFUc17384"				"1.9e-52, 1.0e-67"			
24841	ENU08636	ANI61C8350: 2742..4517			GTBX	CALc06237				2.9E-46			
24842	ENU08637	ANI61C9080: 2749..969			GTBX	"AFUc07425, AFUc19355"				"3.7e-17, 1.2e-21"			

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24844	ENU08639	ANI61C8354: 1395..895			GTBX	"AFUc12206, Y13140"				"3.9e-65, 1.1e-30"			
24845	ENU08640	ANI61C8355: 551..2115			GTBX	"AFUc01781, AFUc01807, AFUc08308"				"1.4e-08, 1.3e-11, 1.6e-22"			
24846	ENU08641	ANI61C7628: 3..290			GTBX	CALc06163				2.5E-28			
24847	ENU08642	ANI61C792:6 85..317			GTBX	AFUc20257				1.8E-38			
24848	ENU08643	ANI61C794:1 079..852			GTBX	AFUc15667				5.6E-29			
24849	ENU08644	ANI61C797:1 521..2941			GTBX	"AFUc12939, AFUc14002"				"3.4e-18, 2.0e-68"			
24850	ENU08645	ANI61C798:5 48..14			GTBX	"AFUc10758, AFUc10988"				"2.2e-36, 9.8e-13"			
24851	ENU08646	ANI61C7633: 311..964			GTBX	AFUc01337				1.1E-46			
24852	ENU08647	ANI61C8363: 497..1386			GTBX	"AFUc15806, AFUc22456, FGRc02315, Y13136"				"5.9e-50, 3.4e-47, 1.0e-46, 3.3e-44"			
24853	ENU08648	ANI61C9092: 198..1162			GTBX	"AFUc15550, U00092"				"7.9e-30, 1.3e-62"			
24854	ENU08649	ANI61C6908: 658..381			GTBX	AFUc11236				2E-80			
24855	ENU08650	ANI61C6910: 1381..152			GTBX	AFUc11952				5E-68			
24856	ENU08651	ANI61C8372: 870..1638			GTBX	"AFUc09758, CALc05309"				"3.5e-77, 2.4e-13"			

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24857	ENU08652	ANI61C8375: 3081..370			GTBX	"AFUc05629, AFUc21466"				"2.3e-91, 1.3e-40"			
24858	ENU08653	ANI61C6919: 239..529			GTBX	AFUc14464				3.6E-35			
24859	ENU08654	ANI61C7649: 949..566			GTBX	AFUc18416				3.9E-25			
24860	ENU08655	ANI61C7651: 786..70			GTBX	CALc05557				1.5E-24			
24861	ENU08656	ANI61C6925: 1425..2330			GTBX	"AFUc04661, AFUc22181"				"2.6e-31, 2.0e-36"			
24862	ENU08657	ANI61C6926: 692..1049			GTBX	AFUc01242				1.3E-46			
24863	ENU08658	ANI61C6927: 3535..2135			GTBX	"AFUc03128, AFUc07465"				"1.8e-65, 5.3e-67"			
24864	ENU08659	ANI61C8385: 3004..3390			GTBX	AFUc09509				3.1E-59			
24865	ENU08660	ANI61C6930: 909..328			GTBX	AFUc07723				3.6E-44			
24866	ENU08661	ANI61C6931: 1816..796			GTBX	AFUc03234				1.2E-51			
24867	ENU08662	ANI61C7661: 1..306			GTBX	AFUc08515				5.1E-41			
24868	ENU08663	ANI61C8391: 1166..822			GTBX	"AFUc02256, AFUc08836"				"2.0e-43, 1.1e-20"			
24869	ENU08664	ANI61C7663: 1683..29			GTBX	"AFUc07074, AFUc11027"				"7.7e-34, 4.4e-29"			
24870	ENU08665	ANI61C7664: 620..1668			GTBX	"CALc05819, FGRc11819, FGRc11819"				"2.1e-66, 1.2e-50, 4.0e-37"			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	Description
24871	ENU08666	ANI61C7665:1405..1690			GTBX	"AFUc20344, FGRc25908"				"3.0e-52, 9.4e-22"			
24872	ENU08667	ANI61C7667:217..764			GTBX	AFUc15868				2.8E-59			
24873	ENU08668	ANI61C7668:546..21			GTBX	AFUc19926				1.1E-48			
24874	ENU08669	ANI61C7669:1362..145			GTBX	"AFUc16122, AFUc18675, CALc06209"				"6.4e-69, 4.8e-37, 4.3e-96"			
24875	ENU08670	ANI61C8398:1256..1657			GTBX	"CALc03932, FGRc14057, FGRc23953"				"4.4e-108, 2.3e-24, 2.2e-44"			
24876	ENU08671	ANI61C6941:2770..1688			GTBX	CALc06022				4E-79			
24877	ENU08672	ANI61C6942:1015..337			GTBX	"AFUc09643, FGRc10423"				"9.0e-22, 6.3e-13"			
24878	ENU08673	ANI61C7672:4149..5074			GTBX	AFUc15338				2.1E-67			
24879	ENU08674	ANI61C7673:2706..3490			GTBX	U00094				4.6e-253			
24880	ENU08675	ANI61C7675:7588..6036			GTBX	"AFUc09612, AFUc18486"				"8.0e-40, 1.4e-39"			
24881	ENU08676	ANI61C6948:514..290			GTBX	AFUc14750				2.7E-34			
24882	ENU08677	ANI61C7689:2240..860			GTBX	AFUc07888				4.6E-109			
24883	ENU08678	ANI61C10:1351..46			GTBX	AFUc04257				9.9E-80			
24884	ENU08679	ANI61C18:28..740			GTBX	AFUc06457				1.5E-24			

Gene Definition

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24885	ENU08680	ANI61C6964:263..6			GTBX	AFUc19698				1.6E-27			
24886	ENU08681	ANI61C7695:1205..3			GTBX	"AFUc14143, FGRc21455"				"2.4e-80, 1.1e-26"			
24887	ENU08682	ANI61C6967:687..361			GTBX	"AFUc15762, AFUc15762"				"1.8e-68, 3.0e-170"			
24888	ENU08683	ANI61C6968:222..943			GTBX	"AFUc08123, CALc05688"				"6.6e-24, 5.1e-87"			
24889	ENU08684	ANI61C6969:1497..1			GTBX	AFUc08629				1.1E-84			
24890	ENU08685	ANI61C21:1021..690			GTBX	"FGRc05811, U00094"				"1.1e-51, 1.2e-97"			
24891	ENU08686	ANI61C24:1302..541			GTBX	AFUc10888				2.2E-38			
24892	ENU08687	ANI61C27:1360..1941			GTBX	CALc04049				5.6E-149			
24893	ENU08688	ANI61C29:1240..77			GTBX	U00094				2.0e-29			
24894	ENU08689	ANI61C6974:1512..1835			GTBX	"AFUc12767, FGRc04567"				"1.8e-09, 1.4e-32"			
24895	ENU08690	ANI61C6976:780..11			GTBX	AFUc20643				5.4E-33			
24896	ENU08691	ANI61C6978:936..477			GTBX	FGRc17293				5E-24			
24897	ENU08692	ANI61C6979:2007..2660			GTBX	AFUc14080				3.3E-22			
24898	ENU08693	ANI61C4002:1132..302			GTBX	AFUc10817				4.7E-59			

Gene Description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24899	ENU08694	ANI61C34:77 8..2349			GTBX	"AFUc10260, FGRc02884, FGRc12117, FGRc19667"				"3.5e-56, 6.5e-48, 5.2e-50, 1.7e-24"			
24900	ENU08695	ANI61C36:77 .634			GTBX	AFUc00656				4.6E-33			
24901	ENU08696	ANI61C6980: 363..1007			GTBX	Y13135				1.2e-31			
24902	ENU08697	ANI61C6985: 625..5			GTBX	"FGRc11412, FGRc17886"				"4.7e-19, 2.8e-36"			
24903	ENU08698	ANI61C6986: 1531..763			GTBX	AFUc12892				1.2E-52			
24904	ENU08699	ANI61C40:84 1..1771			GTBX	AFUc15961				1.2E-45			
24905	ENU08700	ANI61C46:92 8..116			GTBX	AFUc15151				1.5E-77			
24906	ENU08701	ANI61S645:4 1..428			GTBX	AFUc13524				3.1E-39			
24907	ENU08702	ANI61C6999: 887..135			GTBX	AFUc15217				8E-28			
24908	ENU08703	ANI61C4021: 1037..14			GTBX	AFUc00826				1.7E-28			
24909	ENU08704	ANI61C55:10 16..1329			GTBX	AFUc09449				1.8E-23			
24910	ENU08705	ANI61C61:65 60..4412			GTBX	"AFUc07978, FGRc00983, FGRc23299"				"9.0e-24, 2.0e-21, 2.6e-23"			
24911	ENU08706	ANI61C61:96 64..8595			GTBX	AFUc12810				6.1E-33			
24912	ENU08707	ANI61C4034: 490..254			GTBX	FGRc12892				3.8E-40			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24913	ENU08708	ANI61C3307: 997..1236			GTBX	AFUc14556				7.7E-33			
24914	ENU08709	ANI61C3309: 3590..1383			GTBX	"AFUc19897, CALc05545, FGRc10593"				"3.7e-34, 9.3e-107, 6.2e-41" 3.8e-13			
24915	ENU08710	ANI61S3148: 132..339			GTBX	U00094							
24916	ENU08711	ANI61C70:15 4..1477			GTBX	AFUc13679				3.1E-42			
24917	ENU08712	ANI61C74:20 41..1277			GTBX	"FGRc02814, FGRc10359, FGRc18356"				"6.6e-59, 2.0e-50, 1.3e-07" 6.4E-117			
24918	ENU08713	ANI61C3315: 1021..1941			GTBX	AFUc14821							
24919	ENU08714	ANI61C3317: 4317..4820			GTBX	AFUc11811				1E-69			
24920	ENU08715	ANI61C4046: 944..2324			GTBX	AFUc09421				3.9E-37			
24921	ENU08716	ANI61C4047: 816..382			GTBX	AFUc02478				2.6E-45			
24922	ENU08717	ANI61C81:39 81..2518			GTBX	AFUc10625				3E-101			
24923	ENU08718	ANI61C3322: 447..49			GTBX	AFUc19143				1.4E-21			
24924	ENU08719	ANI61C3323: 5065..4721			GTBX	AFUc13265				1.3E-49			
24925	ENU08720	ANI61C84:12 67..794			GTBX	CALc05272				2.5E-47			
24926	ENU08721	ANI61C3328: 10..492			GTBX	Y13136				2.9e-49			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	Description
24927	ENU08722	ANI61C3329: 2681..3493			GTBX	"AFUc16245, AFUc18755"				"1.4e-08, 3.6e-21"			
24928	ENU08723	ANI61C2600: 1242..340			GTBX	"AFUc06261, FGRc12448"				"1.0e-73, 4.7e-46"			
24929	ENU08724	ANI61C3330: 816..12			GTBX	AFUc11045				6.1E-47			
24930	ENU08725	ANI61C4065: 192..470			GTBX	FGRc12294				2.6E-23			
24931	ENU08726	ANI61C3337: 2136..49			GTBX	"AFUc06141, AFUc08576, Y13134"				"1.1e-28, 7.3e-84, 1.6e-61"			
24932	ENU08727	ANI61C3338: 1298..395			GTBX	AFUc09204				1.7E-36			
24933	ENU08728	ANI61C2609: 955..215			GTBX	AFUc10760				4.8E-38			
24934	ENU08729	ANI61C98:15 62..599			GTBX	"AFUc07359, AFUc07383, AFUc15393"				"2.9e-35, 2.8e-60, 1.4e-55"			
24935	ENU08730	ANI61C1140 0:738..1813			GTBX	AFUc15950				2.7E-91			
24936	ENU08731	ANI61C1140 4:4363..3848			GTBX	"AFUc05972, AFUc08582"				"4.6e-27, 3.5e-14"			
24937	ENU08732	ANI61S1712: 90..437			GTBX	"AFUc05166, CALc01912"				"7.1e-13, 1.4e-38"			
24938	ENU08733	ANI61S1715: 46..375			GTBX	AFUc07612				6E-30			
24939	ENU08734	ANI61C3342: 3..452			GTBX	AFUc05841				6.7E-35			
24940	ENU08735	ANI61C3342: 1691..763			GTBX	"AFUc18170, Z71256"				"1.4e-15, 5.6e-14"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24941	ENU08736	ANI61C4072: 1036..572			GTBX	AFUc03577				8.2E-78			
24942	ENU08737	ANI61C2615: 427..2074			GTBX	"AFUc19837, Y13138"				"2.6e-44, 1.4e-41"			
24943	ENU08738	ANI61C3344: 172..816			GTBX	FGRc02406				5.1E-25			
24944	ENU08739	ANI61C2616: 820..2283			GTBX	"AFUc05687, AFUc08664, CALc05800, CALc06229"				"1.7e-49, 7.9e-07, 1.9e-35, 8.4e-26"			
24945	ENU08740	ANI61C4074: 249..872			GTBX	"FGRc11944, U00092"				"4.4e-70, 4.4e-36"			
24946	ENU08741	ANI61C4076: 30..557			GTBX	"AFUc13132, FGRc02840"				"6.1e-32, 2.0e-09"			
24947	ENU08742	ANI61C1141 5:2205..964			GTBX	"AFUc09709, AFUc12435"				"1.5e-66, 6.1e-81"			
24948	ENU08743	ANI61C4080: 37..961			GTBX	AFUc07865				6.1E-73			
24949	ENU08744	ANI61C4082: 632..399			GTBX	AFUc11950				1.1E-26			
24950	ENU08745	ANI61C3355: 619..1088			GTBX	AFUc10222				1.5E-54			
24951	ENU08746	ANI61C3356: 976..367			GTBX	AFUc12958				1.1E-81			
24952	ENU08747	ANI61C3358: 4765..6066			GTBX	AFUc15520				3.1E-70			
24953	ENU08748	ANI61C3359: 1074..440			GTBX	AFUc13793				4.5E-78			
24954	ENU08749	ANI61C1142 2:674..66			GTBX	AFUc07909				2.1E-36			

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24955	ENU08750	ANI61C1142 3:748..1			GTBX	AFUc05597				1.8E-83			
24956	ENU08751	ANI61C1142 7:3870..2475			GTBX	"AFUc08441, FGRc23451, Y13140"				"6.1e-07, 4.6e-12, 4.6e-41"			
24957	ENU08752	ANI61C1142 9:1930..573			GTBX	AFUc06257				1.6E-22			
24958	ENU08753	ANI61C2630: 541..105			GTBX	AFUc08424				3.4E-59			
24959	ENU08754	ANI61C2633: 2625..2233			GTBX	AFUc05841				3.1E-54			
24960	ENU08755	ANI61C4093: 333..85			GTBX	AFUc04043				3.8E-27			
24961	ENU08756	ANI61C2636: 1040..489			GTBX	AFUc11267				4.1E-79			
24962	ENU08757	ANI61C1909: 1..484			GTBX	AFUc13018				2.2E-63			
24963	ENU08758	ANI61C4098: 1484..2175			GTBX	"AFUc12633, AFUc13482, CALc05318"				"5.9e-20, 3.8e-68, 1.2e-10"			
24964	ENU08759	ANI61C1070 0:5786..6253			GTBX	AFUc10021				2.9E-39			
24965	ENU08760	ANI61C1143 0:499..1727			GTBX	AFUc11277				1.9E-64			
24966	ENU08761	ANI61C1143 2:3308..3949			GTBX	"AFUc16152, AFUc16297"				"7.7e-15, 4.1e-26"			
24967	ENU08762	ANI61C1070 4:90..2062			GTBX	"AFUc03602, AFUc18530"				"2.2e-36, 4.7e-60"			
24968	ENU08763	ANI61C1143 5:345..1916			GTBX	"AFUc05782, AFUc15229, FGRc13683"				"1.4e- 122, 2.6e-09, 2.4e-37"			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24983	ENU08778	ANI61C1071 3:1728..3141			GTBX	"AFUc05029, FGRc10887"				"1.9e-28, 1.0e-24"			
24984	ENU08779	ANI61C1144 4:4343..5216			GTBX	"AFUc08298, AFUc22104"				"3.9e-17, 1.2e-23"			
24985	ENU08780	ANI61C1071 6:3219..1252			GTBX	"AFUc09877, AFUc11768, FGRc03217"				"6.4e-52, 4.4e-81, 3.6e-26"			
24986	ENU08781	ANI61C2651: 1167..676			GTBX	AFUc06429				1.4E-47			
24987	ENU08782	ANI61C2653: 670..338			GTBX	FGRc07112				4.2E-45			
24988	ENU08783	ANI61C2654: 823..1444			GTBX	Y13138				2.9e-38			
24989	ENU08784	ANI61C2656: 2061..2360			GTBX	FGRc02646				6.5E-25			
24990	ENU08785	ANI61C1928: 1654..734			GTBX	AFUc12945				5.9E-109			
24991	ENU08786	ANI61C3388: 954..17			GTBX	AFUc08509				2.9E-47			
24992	ENU08787	ANI61C1072 0:565..84			GTBX	AFUc06323				6.2E-26			
24993	ENU08788	ANI61C1072 1:2272..1494			GTBX	AFUc12398				7.6E-75			
24994	ENU08789	ANI61C1072 2:562..1611			GTBX	"AFUc15498, AFUc18421"				"4.6e- 113, 7.1e-50"			
24995	ENU08790	ANI61S1767: 76..593			GTBX	AFUc10191				9.3E-93			
24996	ENU08791	ANI61C1930: 1036..686			GTBX	CALc06119				1.1E-69			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
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24998	ENU08793	ANI61C2660: 1115..1436			GTBX	"AFUc12566, AFUc14338"				"7.5e-40, 3.9e-35"			
24999	ENU08794	ANI61C1933: 1613..1178			GTBX	AFUc07117				3.2E-66			
25000	ENU08795	ANI61C3397: 3091..1810			GTBX	"AFUc11193, AFUc11193, FGRc03055"				"1.4e-43, 1.4e-59, 8.1e-12"			
25001	ENU08796	ANI61C1073 7:1325..2336			GTBX	"AFUc18885, CALc04126, Y13140"				"3.5e-44, 1.8e-25, 9.6e-35"			
25002	ENU08797	ANI61C1146 7:385..858			GTBX	AFUc19804				3.5E-37			
25003	ENU08798	ANI61C1146 7:2860..1414			GTBX	"AFUc09725, CALc06090"				"7.7e-53, 2.6e-08"			
25004	ENU08799	ANI61C1941: 105..1823			GTBX	"CALc05195, FGRc16068, Y13138"				"2.7e-31, 1.7e-37, 2.1e-97"			
25005	ENU08800	ANI61C2670: 1338..683			GTBX	"AFUc08344, FGRc03704"				"2.7e-31, 3.7e-101"			
25006	ENU08801	ANI61C1943: 20..484			GTBX	AFUc11732				1.9E-76			
25007	ENU08802	ANI61C2673: 769..30			GTBX	"AFUc13809, CALc05583"				"3.6e-71, 1.4e-64"			
25008	ENU08803	ANI61C1946: 647..3			GTBX	FGRc10049				8.7E-42			
25009	ENU08804	ANI61C2676: 1204..362			GTBX	AFUc13919				6.5E-148			
25010	ENU08805	ANI61C2679: 1853..2069			GTBX	Y13138				2.4e-23			

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25012	ENU08807	ANI61C1074 1:1607..918			GTBX	AFUc14682				1.9E-80			
25013	ENU08808	ANI61C1147 1:2164..1046			GTBX	AFUc03516				1E-25			
25014	ENU08809	ANI61C1074 2:1908..2430			GTBX	AFUc06521				1.9E-43			
25015	ENU08810	ANI61C1147 8:1292..2764			GTBX	AFUc14969				6.3E-198			
25016	ENU08811	ANI61C1952: 2185..3687			GTBX	"AFUc14718, FGRc15556"				"4.9e- 131, 9.1e-41" 8.4E-87			
25017	ENU08812	ANI61C1957: 1467..1747			GTBX	AFUc14883				1E-44			
25018	ENU08813	ANI61C1075 0:1589..2369			GTBX	AFUc14574				4.6E-32			
25019	ENU08814	ANI61C1148 1:482..35			GTBX	AFUc11691				1.5E-24			
25020	ENU08815	ANI61C1075 3:141..476			GTBX	AFUc15229				1.8E-26			
25021	ENU08816	ANI61C1960: 1871..1443			GTBX	AFUc04303				2.8E-128			
25022	ENU08817	ANI61C2692: 3428..2316			GTBX	AFUc09746				1.8E-45			
25023	ENU08818	ANI61C2693: 449..95			GTBX	AFUc13804				"6.5e-27, 4.2e-61"			
25024	ENU08819	ANI61C2698: 745..259			GTBX	"AFUc07690, AFUc12854"							

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25025	ENU08820	ANI61C2698:1594..988			GTBX	"AFUc09690, AFUc12854, FGRc07517"				"2.8e-25, 4.2e-61, 1.6e-18"			
25026	ENU08821	ANI61C1076 4:709..109			GTBX	"CALc05408, FGRc05636"				"2.6e-24, 2.2e-25"			
25027	ENU08822	ANI61C1076 7:2475..3500			GTBX	AFUc11524				3.5E-85			
25028	ENU08823	ANI61C1972:1158..691			GTBX	ZA7047				8.1e-21			
25029	ENU08824	ANI61C1973:128..544			GTBX	AFUc15874				8.6E-34			
25030	ENU08825	ANI61C1974:196..552			GTBX	AFUc14463				2.7E-47			
25031	ENU08826	ANI61C1975:2720..6			GTBX	"AFUc11768, AFUc14088, AFUc14691, FGRc19856"				"1.2e-72, 7.4e-92, 9.9e-72, 1.3e-13"			
25032	ENU08827	ANI61C807:104..363			GTBX	FGRc08860				1.3E-23			
25033	ENU08828	ANI61C809:397..740			GTBX	AFUc15761				9.8E-56			
25034	ENU08829	ANI61C1077 6:4764..5669			GTBX	AFUc14848				2.3E-87			
25035	ENU08830	ANI61C9100:1569..543			GTBX	AFUc10383				4.6E-54			
25036	ENU08831	ANI61C9104:5043..5687			GTBX	"AFUc03688, FGRc07492"				"9.0e-27, 1.5e-26"			
25037	ENU08832	ANI61C9105:1952..601			GTBX	AFUc05381				3.2E-57			
25038	ENU08833	ANI61C9107:3660..5664			GTBX	"AFUc13126, FGRc07962"				"5.8e-55, 5.9e-42"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25039	ENU08834	ANI61C1818:3 256..2912			GTBX	FGRc24873				4.6E-41			
25040	ENU08835	ANI61C1078 8:1519..49			GTBX	FGRc09740				3.1E-28			
25041	ENU08836	ANI61C1078 9:1896..1027			GTBX	AFUc13090				3.1E-114			
25042	ENU08837	ANI61C9112: 2215..3174			GTBX	AFUc05724				7.5E-81			
25043	ENU08838	ANI61C9112: 4794..3825			GTBX	AFUc12748				1.9E-60			
25044	ENU08839	ANI61C9117: 4650..5342			GTBX	AFUc22177				4.9E-54			
25045	ENU08840	ANI61C9118: 2481..4081			GTBX	"AFUc05152, AFUc06401"				"3.3e-67, 4.0e-15"			
25046	ENU08841	ANI61C822:9 78..138			GTBX	AFUc05328				2.1E-37			
25047	ENU08842	ANI61C826:4 55..1470			GTBX	"AFUc06686, AFUc11073"				"1.3e-44, 1.5e-19"			
25048	ENU08843	ANI61C827:1 030..74			GTBX	"AFUc12162, AFUc19854"				"2.2e-62, 5.0e-45"			
25049	ENU08844	ANI61C828:2 324..2715			GTBX	AFUc02177				1.4E-38			
25050	ENU08845	ANI61C1079 2:295..726			GTBX	"AFUc03882, FGRc06121"				"1.9e-40, 7.0e-35"			
25051	ENU08846	ANI61C1079 6:1764..38			GTBX	"AFUc04821, Y13138"				"4.2e- 100, 7.6e- 120"			
25052	ENU08847	ANI61C9125: 1139..627			GTBX	AFUc12750				2E-36			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25053	ENU08848	ANI61C836:8 95..335			GTBX	"AFUc14883, AFUc14883"				"5.8e-46, 7.5e-53"			
25054	ENU08849	ANI61C837:4 1..566			GTBX	AFUc20588				3.6E-38			
25055	ENU08850	ANI61C8403: 2265..1942			GTBX	AFUc08360				7.3E-22			
25056	ENU08851	ANI61C8406: 3383..1653			GTBX	"AFUc12104, AFUc15297, Y13135"				"4.0e-62, 3.7e-23, 3.0e-46"			
25057	ENU08852	ANI61C9136: 666..908			GTBX	AFUc13948				5.9E-32			
25058	ENU08853	ANI61C8407: 2066..705			GTBX	"AFUc13751, AFUc13751"				"3.4e- 186, 6.1e- 210"			
25059	ENU08854	ANI61C848:1 328..2315			GTBX	AFUc08609				1.7E-86			
25060	ENU08855	ANI61C8411: 739..2328			GTBX	"CALc05880, D50617"				"3.4e-96, 2.2e-48"			
25061	ENU08856	ANI61C8413: 1811..1191			GTBX	"AFUc07925, Y13139"				"1.6e- 105, 2.0e-95"			
25062	ENU08857	ANI61C8414: 79..1278			GTBX	"AFUc01427, FGRc11796"				"1.1e-07, 3.1e-73"			
25063	ENU08858	ANI61C8418: 1559..1860			GTBX	AFUc13723				3.3E-33			
25064	ENU08859	ANI61C8419: 1451..2381			GTBX	"AFUc08249, FGRc12401"				"2.7e- 159, 1.8e-23"			
25065	ENU08860	ANI61C9149: 2758..2324			GTBX	AFUc02271				1.4E-50			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	Description
25066	ENU08861	ANI61C851:1 029..1701			GTBX	FGRc06929				3.6E-28			
25067	ENU08862	ANI61C853:7 64..1566			GTBX	AFUc12396				9.4E-77			
25068	ENU08863	ANI61C855:7 0..519			GTBX	"AFUc12828, FGRc08325"				"2.8e-34, 1.4e-22"			
25069	ENU08864	ANI61C857:2 364..1240			GTBX	AFUc21112				4.9E-55			
25070	ENU08865	ANI61C9154: 1083..30			GTBX	AFUc10496				1.8E-45			
25071	ENU08866	ANI61C8429: 1639..1370			GTBX	AFUc09889				1.4E-68			
25072	ENU08867	ANI61C867:9 93..1			GTBX	Y13135				2.2e-20			
25073	ENU08868	ANI61C7703: 1506..530			GTBX	"AFUc11864, AFUc13604, AFUc15296"				"4.3e-21, 7.0e-54, 4.0e-20"			
25074	ENU08869	ANI61C7704: 1011..306			GTBX	FGRc20146				3.6E-34			
25075	ENU08870	ANI61C8433: 3..374			GTBX	AFUc14422				1.3E-50			
25076	ENU08871	ANI61C8436: 1397..1989			GTBX	AFUc12944				1.3E-83			
25077	ENU08872	ANI61C7709: 812..115			GTBX	FGRc12224				1.6E-70			
25078	ENU08873	ANI61C875:2 057..1446			GTBX	Y13135				6.9e-17			
25079	ENU08874	ANI61C8441: 1416..541			GTBX	FGRc12904				2.8E-24			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25080	ENU08875	ANI61C7714: 1136..2228			GTBX	"FGRc06342, FGRc14811"				"8.4e-13, 6.0e-22"			
25081	ENU08876	ANI61C8446: 620..29			GTBX	"AFUc11909, FGRc12199"				"3.5e-19, 7.9e-38"			
25082	ENU08877	ANI61C7717: 1113..1711			GTBX	AFUc07025				3.2E-41			
25083	ENU08878	ANI61C7717: 5981..5119			GTBX	"AFUc16351, FGRc04611"				"4.4e-23, 7.7e-20"			
25084	ENU08879	ANI61C9179: 3890..5546			GTBX	"AFUc13046, AFUc22205"				"7.7e-96, 9.1e-37"			
25085	ENU08880	ANI61C886:5 224..3674			GTBX	"AFUc04165, AFUc14221"				"5.2e-09, 9.9e-39"			
25086	ENU08881	ANI61C888:4 222..3713			GTBX	AFUc20805				2.2E-28			
25087	ENU08882	ANI61C7721: 563..1320			GTBX	"AFUc12977, AFUc14414"				"6.6e-33, 6.6e-17"			
25088	ENU08883	ANI61C7724: 45..794			GTBX	AFUc10173				3.6E-116			
25089	ENU08884	ANI61C8456: 2127..40			GTBX	"AFUc09795, Z71256"				"7.6e-59, 6.7e-212"			
25090	ENU08885	ANI61C9189: 1464..940			GTBX	AFUc00837				8.5E-38			
25091	ENU08886	ANI61C894:1 514..653			GTBX	AFUc15628				4.7E-69			
25092	ENU08887	ANI61C9190: 1512..525			GTBX	"FGRc00983, FGRc26079"				"3.9e-44, 5.8e-18"			
25093	ENU08888	ANI61C8463: 815..1153			GTBX	AFUc11295				5.4E-117			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25094	ENU08889	ANI61C7735: 367..666			GTBX	AFUc12028				5.3E-40			
25095	ENU08890	ANI61C7736: 25..516			GTBX	FGRc25728				4.5E-41			
25096	ENU08891	ANI61C9196: 509..1774			GTBX	"AFUc05790, AFUc13990, FGRc15154"				"2.0e-29, 1.8e-29, 3.4e-25"			
25097	ENU08892	ANI61C7739: 947..600			GTBX	FGRc14654				2.7E-22			
25098	ENU08893	ANI61C9198: 816..496			GTBX	AFUc09614				2.3E-27			
25099	ENU08894	ANI61C8469: 1100..398			GTBX	"AFUc18110, FGRc17629"				"3.2e-58, 3.5e-11"			
25100	ENU08895	ANI61C8470: 1108..629			GTBX	AFUc02394				1.1E-22			
25101	ENU08896	ANI61C7741: 2522..4541			GTBX	"AFUc13489, AFUc17708, CALc05924"				"1.9e-19, 1.5e-38, 6.9e-239"			
25102	ENU08897	ANI61C8475: 731..1763			GTBX	AFUc21062				3.5E-43			
25103	ENU08898	ANI61C7756: 1266..573			GTBX	"CALc05253, FGRc26927"				"7.8e-60, 1.4e-15"			
25104	ENU08899	ANI61C8486: 2739..3881			GTBX	"AFUc12062, AFUc14671"				"1.9e-102, 3.9e-98"			
25105	ENU08900	ANI61C8487: 2372..427			GTBX	AFUc15656				1.1E-244			
25106	ENU08901	ANI61C7759: 141..404			GTBX	CALc04035				1.6E-33			

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25107	ENU08902	ANI61C8490:171..1778			GTBX	"CALc05635, FGRc06214, FGRc20613"				"9.5e-66, 4.0e-20, 9.4e-68"			
25108	ENU08903	ANI61C7762:584..1			GTBX	AFUc10277				6E-91			
25109	ENU08904	ANI61C7765:763..57			GTBX	Z71256				7.6e-26			
25110	ENU08905	ANI61C7766:86..706			GTBX	AFUc02641				2.8E-22			
25111	ENU08906	ANI61C7767:4855..4230			GTBX	AFUc21500				2.9E-46			
25112	ENU08907	ANI61C7768:3372..3915			GTBX	AFUc15315				1.9E-112			
25113	ENU08908	ANI61C7770:989..79			GTBX	AFUc03608				4.9E-58			
25114	ENU08909	ANI61S14:618..264			GTBX	"FGRc00672, FGRc09713"				"9.2e-07, 2.9e-37"			
25115	ENU08910	ANI61C7771:4802..3214			GTBX	"AFUc01209, AFUc05079"				"4.0e-28, 3.9e-16"			
25116	ENU08911	ANI61C7773:503..1698			GTBX	"AFUc02171, FGRc00650"				"3.1e-32, 3.4e-14"			
25117	ENU08912	ANI61C7774:3657..2305			GTBX	AFUc01162				5.6E-121			
25118	ENU08913	ANI61C7777:1063..1767			GTBX	"AFUc05844, FGRc12412"				"8.7e-74, 4.4e-30"			
25119	ENU08914	ANI61C7786:232..921			GTBX	AFUc05158				3.6E-50			
25120	ENU08915	ANI61C7789:735..1117			GTBX	AFUc14811				7.1E-29			

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25121	ENU08916	ANI61S719:4 58..168			GTBX	AFUc05321				1E-29			
25122	ENU08917	ANI61C7792: 207..1448			GTBX	"AFUc15949, FGRc07097"				"3.3e-38, 7.1e-24"			
25123	ENU08918	ANI61C4102: 1585..1031			GTBX	AFUc14601				9.8E-63			
25124	ENU08919	ANI61C4103: 891..301			GTBX	"AFUc02035, AFUc18244, FGRc16341"				"6.8e-16, 6.3e-49, 1.0e-12"			
25125	ENU08920	ANI61C4106: 888..1172			GTBX	AFUc12497				6.4E-29			
25126	ENU08921	ANI61C4107: 3073..4246			GTBX	"AFUc03644, AFUc03949, AFUc07144"				"2.3e-51, 1.8e-29, 3.7e-22"			
25127	ENU08922	ANI61C4107: 6848..4563			GTBX	"AFUc10284, AFUc16568, FGRc23371"				"3.4e-124, 1.8e-25, 4.3e-10"			
25128	ENU08923	ANI61C4108: 1056..2837			GTBX	"AFUc05077, AFUc15554, FGRc08841"				"2.6e-43, 5.2e-121, 4.0e-59"			
25129	ENU08924	ANI61S51:11. .352			GTBX	AFUc09974				4.7E-50			
25130	ENU08925	ANI61C4116: 565..195			GTBX	"AFUc14805, AFUc20877"				"6.4e-36, 4.6e-38"			
25131	ENU08926	ANI61C4119: 741..313			GTBX	AFUc06070				1E-39			
25132	ENU08927	ANI61C4124: 2482..2991			GTBX	AFUc11634				4.7E-39			

Contig source

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	Description
25146	ENU08941	ANI61C4154:750..427			GTBX	FGRc08165							
25147	ENU08942	ANI61C3426:799..1035			GTBX	AFUc14425							
25148	ENU08943	ANI61C4156:811..158			GTBX	AFUc01911							
25149	ENU08944	ANI61C4164:1102..2126			GTBX	"AFUc07502, CALc06043"							
25150	ENU08945	ANI61C4165:2879..2147			GTBX	AFUc05660							
25151	ENU08946	ANI61C3439:1918..547			GTBX	AFUc08088							
25152	ENU08947	ANI61S798:2..358			GTBX	AFUc06449							
25153	ENU08948	ANI61S3272:1..396			GTBX	AFUc06662							
25154	ENU08949	ANI61C3442:978..2365			GTBX	"AFUc15654, AFUc15654"							
25155	ENU08950	ANI61C3444:1126..196			GTBX	AFUc04760							
25156	ENU08951	ANI61C4177:622..1022			GTBX	AFUc06724							
25157	ENU08952	ANI61C2723:2..913			GTBX	AFUc15132							
25158	ENU08953	ANI61C2724:875..213			GTBX	AFUc15688							
25159	ENU08954	ANI61C2726:574..30			GTBX	CALc05920							

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25160	ENU08955	ANI61C4187: 379..1145			GTBX	AFUc14608				1.2E-83			
25161	ENU08956	ANI61C3458: 1001..567			GTBX	AFUc10128				4.9E-42			
25162	ENU08957	ANI61C3459: 669..199			GTBX	AFUc12576				4.2E-60			
25163	ENU08958	ANI61S1831: 532..19			GTBX	FGRc00578				1.1E-29			
25164	ENU08959	ANI61S1834: 390..665			GTBX	AFUc11038				1.9E-63			
25165	ENU08960	ANI61S2569: 41..484			GTBX	FGRc24279				2.8E-35			
25166	ENU08961	ANI61C3460: 1017..1299			GTBX	AFUc13761				2E-109			
25167	ENU08962	ANI61C3461: 849..64			GTBX	"AFUc00703, AFUc13932"				"1.6e-11, 2.8e-64"			
25168	ENU08963	ANI61C4191: 1298..198			GTBX	AFUc07701				6.1E-56			
25169	ENU08964	ANI61C4195: 1387..1874			GTBX	AFUc11252				5.6E-91			
25170	ENU08965	ANI61C2738: 853..278			GTBX	"FGRc06990, Z71257"				"6.1e-15, 1.5e-33"			
25171	ENU08966	ANI61C4198: 582..151			GTBX	AFUc01658				6.5E-35			
25172	ENU08967	ANI61C1080 6:191..656			GTBX	"AFUc07431, AFUc13621"				"9.6e-15, 1.4e-57"			
25173	ENU08968	ANI61C1080 7:5457..6306			GTBX	"AFUc01138, CALc03518"				"3.6e-08, 3.8e-33"			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25174	ENU08969	ANI61C3470: 1388..1606			GTBX	AFUc07764				9.6E-105			
25175	ENU08970	ANI61C3473: 772..392			GTBX	AFUc18497				6.7E-24			
25176	ENU08971	ANI61C3475: 3209..3995			GTBX	AFUc05872				9.5E-50			
25177	ENU08972	ANI61C2747: 43..471			GTBX	AFUc14390				2.1E-34			
25178	ENU08973	ANI61C1081 2:1544..3776			GTBX	"AFUc13531, AFUc14233, AFUc14327, AFUc14338"				"3.9e-29, 2.4e-31, 9.0e-57, 3.8e-50"			
25179	ENU08974	ANI61C1081 4:545..141			GTBX	"AFUc09407, FGRC11267"				"3.5e-23, 4.1e-07"			
25180	ENU08975	ANI61S1855: 51..573			GTBX	AFUc14395				7.2E-32			
25181	ENU08976	ANI61C2753: 713..1036			GTBX	AFUc12177				4.6E-28			
25182	ENU08977	ANI61C3482: 1159..1505			GTBX	"AFUc08947, Y13137"				"3.6e-76, 2.1e-44"			
25183	ENU08978	ANI61C2754: 1..520			GTBX	AFUc11200				1.1E-29			
25184	ENU08979	ANI61C3487: 334..1136			GTBX	AFUc21091				1.2E-22			
25185	ENU08980	ANI61C2758: 96..608			GTBX	FGRC12220				7.4E-48			
25186	ENU08981	ANI61C2763: 1297..582			GTBX	"AFUc13692, AFUc13754"				"5.8e-77, 4.6e-43"			
25187	ENU08982	ANI61C3497: 38..559			GTBX	FGRC10471				6.1E-74			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25188	ENU08983	ANI61C1083 6:2079..834			GTBX	"AFUc14311, AFUc22325"				"1.8e-106, 1.3e-30" 8.8E-23			
25189	ENU08984	ANI61C2777: 249..27			GTBX	AFUc09165							
25190	ENU08985	ANI61C1084 2:263..21			GTBX	AFUc15294				1.5E-26			
25191	ENU08986	ANI61C1084 6:2234..3543			GTBX	"AFUc14245, CALc05322, Y13140"				"9.0e-161, 5.3e-60, 5.3e-108" "8.3e-21, 1.3e-24" 4.5E-54			
25192	ENU08987	ANI61C1084 8:416..3			GTBX	"AFUc21087, CALc06090"							
25193	ENU08988	ANI61C1084 9:3548..4105			GTBX	AFUc10042							
25194	ENU08989	ANI61C2783: 1271..2181			GTBX	AFUc08854				1.3E-97			
25195	ENU08990	ANI61C2791: 906..498			GTBX	AFUc14237				2.6E-38			
25196	ENU08991	ANI61C2792: 876..36			GTBX	AFUc16118				1.2E-34			
25197	ENU08992	ANI61C2794: 1584..1084			GTBX	AFUc13519				5.2E-35			
25198	ENU08993	ANI61C2799: 1320..1669			GTBX	AFUc14105				2.7E-43			
25199	ENU08994	ANI61C1086 2:1103..489			GTBX	AFUc13456				5.7E-82			
25200	ENU08995	ANI61C1086 9:1089..200			GTBX	"AFUc12779, AFUc12779"				"1.0e-29, 1.0e-37"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25201	ENU08996	ANI61C1087 2:2004..2818			GTBX	"CALc05217, Y13138"				"1.9e-159, 5.5e-211"			
25202	ENU08997	ANI61C1087 3:1155..2865			GTBX	"CALc03654, X59720"				"1.5e-46, 2.0e-50"			
25203	ENU08998	ANI61C1087 4:3565..4204			GTBX	AFUc15811				1.1E-83			
25204	ENU08999	ANI61C1087 5:82..2501			GTBX	"AFUc04817, AFUc21485, FGRc09205"				"1.9e-69, 7.3e-13, 3.3e-22"			
25205	ENU09000	ANI61C9200: 1423..2081			GTBX	AFUc15632				1.4E-33			
25206	ENU09001	ANI61C9201: 617..383			GTBX	AFUc08928				7.5E-42			
25207	ENU09002	ANI61C9203: 4520..63			GTBX	"AFUc09601, AFUc13531, AFUc15132, AFUc19875"				"1.1e-32, 4.6e-40, 5.1e-48, 1.4e-22"			
25208	ENU09003	ANI61C9206: 770..81			GTBX	AFUc08110				1E-27			
25209	ENU09004	ANI61C9207: 3570..1397			GTBX	"AFUc15140, AFUc15140, AFUc19221"				"1.7e-141, 2.8e-29, 4.6e-48"			
25210	ENU09005	ANI61C914:4 504..3529			GTBX	"AFUc09101, CALc01241, FGRc07803"				"9.2e-51, 2.8e-29, 2.3e-25"			
25211	ENU09006	ANI61C918:1 53..1052			GTBX	AFUc11011				6.2E-58			
25212	ENU09007	ANI61C9211: 2395..3456			GTBX	"AFUc14615, AFUc22530"				"3.1e-51, 9.2e-42"			
25213	ENU09008	ANI61C9215: 1494..1788			GTBX	AFUc00720				9.1E-26			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	% Description
25214	ENU09009	ANI61C9216: 2755..1219			GTBX	"AFUc14313, AFUc14313"				"1.1e-160, 1.6e-157"			
25215	ENU09010	ANI61C923:6 85..239			GTBX	FGRc06929				5.2E-27			
25216	ENU09011	ANI61C1089 2:2598..1435			GTBX	"AFUc03032, AFUc05892, Y13140"				"4.4e-43, 5.3e-16, 5.4e-18"			
25217	ENU09012	ANI61C9227: 49..1215			GTBX	"AFUc09616, FGRc06065"				"3.1e-106, 5.0e-45"			
25218	ENU09013	ANI61C9229: 44..629			GTBX	AFUc20770				1.3E-32			
25219	ENU09014	ANI61C931:4 332..1795			GTBX	"AFUc06172, AFUc06611"				"6.7e-29, 3.0e-41"			
25220	ENU09015	ANI61C8503: 4176..4553			GTBX	FGRc01667				2.7E-21			
25221	ENU09016	ANI61C8508: 1008..2044			GTBX	"AFUc11315, CALc04402"				"7.7e-85, 4.4e-53"			
25222	ENU09017	ANI61C9237: 282..2495			GTBX	Y13134				8.0e-80			
25223	ENU09018	ANI61C948:1 06..598			GTBX	AFUc19097				3.3E-34			
25224	ENU09019	ANI61C9240: 1748..61			GTBX	"AFUc15932, AFUc15932"				"2.9e-38, 3.7e-47"			
25225	ENU09020	ANI61C8511: 892..413			GTBX	AFUc13528				8E-52			
25226	ENU09021	ANI61C8517: 556..35			GTBX	FGRc00709				6.1E-30			
25227	ENU09022	ANI61C9247: 2593..1793			GTBX	AFUc01187				2.4E-29			

Table 6. Contigs

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25228	ENU09023	ANI61C8519:1036..209			GTBX	AFUc11611				6E-54			
25229	ENU09024	ANI61C953:912..1			GTBX	AFUc13929				4.2E-68			
25230	ENU09025	ANI61C957:22..627			GTBX	AFUc14610				1.8E-80			
25231	ENU09026	ANI61C8522:2171..1635			GTBX	AFUc02919				2.5E-49			
25232	ENU09027	ANI61C9253:2222..3333			GTBX	"AFUc05780, FGRc20446"				"1.4e-15, 3.6e-23"			
25233	ENU09028	ANI61C8526:841..65			GTBX	"AFUc09020, Y13136"				"2.0e-41, 7.5e-31"			
25234	ENU09029	ANI61C8526:4617..5334			GTBX	"AFUc21180, CALc04630"				"4.4e-40, 8.5e-22"			
25235	ENU09030	ANI61C9257:1241..480			GTBX	CALc05995				1.4E-53			
25236	ENU09031	ANI61C8531:3577..3233			GTBX	AFUc07659				2.6E-27			
25237	ENU09032	ANI61C8533:2549..1044			GTBX	AFUc06933				8.6E-41			
25238	ENU09033	ANI61C9265:8351..8701			GTBX	AFUc13733				2.4E-119			
25239	ENU09034	ANI61C7807:752..321			GTBX	AFUc15441				2.4E-34			
25240	ENU09035	ANI61C973:607..278			GTBX	FGRc18829				6.4E-22			
25241	ENU09036	ANI61C975:70..423			GTBX	AFUc04456				3.4E-33			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25242	ENU09037	ANI61C976:5 01..755			GTBX	"AFUc08733, AFUc10087"				"1.9e-31, 1.3e-67"			
25243	ENU09038	ANI61C978:7 61..18			GTBX	"AFUc02805, AFUc21089"				"3.5e-45, 8.0e-26"			
25244	ENU09039	ANI61C8542: 2..313			GTBX	AFUc16158				7.5E-31			
25245	ENU09040	ANI61C7814: 2279..2073			GTBX	U00092				2.9e-11			
25246	ENU09041	ANI61C8544: 6230..7238			GTBX	"AFUc02018, AFUc15483, AFUc15778"				"7.4e-51, 9.7e-18, 3.9e-26"			
25247	ENU09042	ANI61C7817: 2093..38			GTBX	"AFUc12368, AFUc15695, AFUc15695"				"2.6e-82, 1.1e-30, 3.1e-12"			
25248	ENU09043	ANI61C8547: 2244..2879			GTBX	"AFUc03289, AFUc12872"				"1.2e-08, 1.9e-31"			
25249	ENU09044	ANI61C7825: 1907..493			GTBX	"AFUc07632, AFUc16753, CALc05461"				"2.4e-80, 3.7e-25, 5.1e-25"			
25250	ENU09045	ANI61C7827: 166..912			GTBX	AFUc15752				3.3E-134			
25251	ENU09046	ANI61C992:2 850..3833			GTBX	"AFUc08206, AFUc13826"				"2.1e-21, 4.5e-77"			
25252	ENU09047	ANI61C8562: 871..199			GTBX	AFUc13633				5E-74			
25253	ENU09048	ANI61C8565: 637..1002			GTBX	FGRc02523				4.8E-30			
25254	ENU09049	ANI61C9295: 1450..440			GTBX	"AFUc08217, FGRc09703"				"1.7e-83, 6.6e-23"			
25255	ENU09050	ANI61C8566: 770..39			GTBX	"AFUc15765, CALc05653"				"8.4e-56, 4.2e-83"			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25256	ENU09051	ANI61C8568: 1119..68			GTBX	AFUc03216				4.1E-61			
25257	ENU09052	ANI61C9298: 815..18			GTBX	"AFUc14355, AFUc22510"				"5.1e-25, 5.2e-74"			
25258	ENU09053	ANI61C9299: 657..1844			GTBX	"AFUc00708, AFUc09276"				"3.5e-38, 3.5e-49"			
25259	ENU09054	ANI61C7844: 946..392			GTBX	AFUc15765				3.5E-112			
25260	ENU09055	ANI61C8574: 1601..2681			GTBX	"AFUc06883, FGRc14811"				"3.7e-79, 6.3e-13"			
25261	ENU09056	ANI61C7847: 931..2031			GTBX	"AFUc10607, U00094"				"1.6e-61, 1.1e-32"			
25262	ENU09057	ANI61C7849: 4332..4955			GTBX	"AFUc03724, FGRc24839"				"5.3e-29, 1.9e-21"			
25263	ENU09058	ANI61C8580: 10232..10627			GTBX	AFUc06423				8.9E-30			
25264	ENU09059	ANI61C8584: 101..535			GTBX	Y13140				2.3e-12			
25265	ENU09060	ANI61C7855: 2920..4065			GTBX	AFUc12170				1.4E-123			
25266	ENU09061	ANI61C7855: 6507..4837			GTBX	AFUc19366				5.1E-49			
25267	ENU09062	ANI61C7857: 488..1039			GTBX	AFUc02328				5.9E-22			
25268	ENU09063	ANI61C7864: 3045..3936			GTBX	"AFUc03531, AFUc12810"				"3.9e-21, 3.2e-20"			
25269	ENU09064	ANI61C8596: 2092..2			GTBX	"AFUc03147, CALc06221, Z71257"				"1.4e-13, 8.8e-21, 2.0e-143"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25311	ENU09106	ANI61C4285: 2704..4107			GTBX	AFUc07246				3.2E-153			
25312	ENU09107	ANI61C3557: 107..924			GTBX	AFUc13932				2.7E-33			
25313	ENU09108	ANI61C3558: 1507..913			GTBX	"FGRc09765, Y13135"				"7.1e-33, 3.2e-53"			
25314	ENU09109	ANI61C2834: 1324..253			GTBX	"AFUc14023, AFUc18413, FGRc11244"				"2.3e-36, 1.6e-52, 8.8e-07"			
25315	ENU09110	ANI61C3565: 80..1109			GTBX	"AFUc12638, AFUc14019"				"3.6e-94, 1.7e-19"			
25316	ENU09111	ANI61C2836: 842..1150			GTBX	AFUc09693				3.9E-47			
25317	ENU09112	ANI61C4295: 526..2590			GTBX	"AFUc14660, AFUc15941, AFUc15941"				"2.9e-12, 4.1e-55, 6.5e-45"			
25318	ENU09113	ANI61C3569: 22..474			GTBX	AFUc01238				1.1E-22			
25319	ENU09114	ANI61C1090 0:246..490			GTBX	FGRc11747				9.5E-32			
25320	ENU09115	ANI61C1090 1:24..497			GTBX	AFUc13935				3.6E-65			
25321	ENU09116	ANI61C3570: 607..1650			GTBX	"CALc05316, U00094"				"2.9e-10, 1.1e-41"			
25322	ENU09117	ANI61C3578: 68..364			GTBX	AFUc04929				9.7E-23			
25323	ENU09118	ANI61C1091 2:864..129			GTBX	AFUc15752				1.8E-26			
25324	ENU09119	ANI61C1091 6:1704..605			GTBX	AFUc14099				1.1E-29			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25325	ENU09120	ANI61C2852:1722..1			GTBX	"AFUc10454, AFUc14364, CALc03886"				"3.9e-33, 3.7e-94, 6.7e-58"			
25326	ENU09121	ANI61C3582:1760..305			GTBX	AFUc09771				6.3E-23			
25327	ENU09122	ANI61C2856:623..366			GTBX	CALc06129				1.1E-37			
25328	ENU09123	ANI61C3587:576..272			GTBX	AFUc17615				1.5E-30			
25329	ENU09124	ANI61C10927:603..24			GTBX	AFUc14337				8.9E-30			
25330	ENU09125	ANI61S2694:358..12			GTBX	FGRc08083				1.3E-39			
25331	ENU09126	ANI61C2860:743..120			GTBX	FGRc01600				7.9E-57			
25332	ENU09127	ANI61C3590:2212..1250			GTBX	AFUc01539				5.3E-59			
25333	ENU09128	ANI61C2864:234..450			GTBX	FGRc05834				1.2E-23			
25334	ENU09129	ANI61C2866:400..2			GTBX	AFUc06319				6.3E-54			
25335	ENU09130	ANI61C3596:508..8			GTBX	AFUc09790				4.4E-62			
25336	ENU09131	ANI61C10931:1458..1075			GTBX	AFUc09609				1.7E-30			
25337	ENU09132	ANI61C10932:2674..1592			GTBX	"AFUc16521, AFUc16612"				"1.2e-23, 2.8e-09"			
25338	ENU09133	ANI61C10934:2128..413			GTBX	"AFUc16639, FGRc02861, FGRc09286, FGRc11948"				"1.1e-81, 1.6e-60, 1.3e-56, 6.3e-08"			

GenBank Accession

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25339	ENU09134	ANI61C1093 7:1836..2395			GTBX	AFUc04964				1.3E-86			
25340	ENU09135	ANI61C1094 6:1623..629			GTBX	"AFUc07110, AFUc18195"				"6.0e-77, 1.6e-11"			
25341	ENU09136	ANI61C2889: 806..204			GTBX	AFUc12218				5.6E-93			
25342	ENU09137	ANI61C1095 4:2579..3314			GTBX	Y13139				1.7e-39			
25343	ENU09138	ANI61C1095 5:532..42			GTBX	AFUc18408				3.1E-33			
25344	ENU09139	ANI61C1095 5:777..2889			GTBX	AFUc13607				5.8E-159			
25345	ENU09140	ANI61C2891: 102..356			GTBX	AFUc07028				4.3E-80			
25346	ENU09141	ANI61C1096 4:14..1231			GTBX	"AFUc11060, AFUc15343"				"3.8e-59, 5.7e-32"			
25347	ENU09142	ANI61C1097 0:2035..312			GTBX	"AFUc12156, AFUc15465, AFUc15465, FGRc00470"				"4.9e-55, 1.5e-10, 2.5e-45, 5.6e-11" 4.3E-55			
25348	ENU09143	ANI61C1097 4:2482..3605			GTBX	AFUc13816							
25349	ENU09144	ANI61C1097 4:9381..10970			GTBX	CALc05781				1.6E-108			
25350	ENU09145	ANI61C1097 5:827..1721			GTBX	AFUc16580				6.4E-29			
25351	ENU09146	ANI61C1097 5:7763..8178			GTBX	FGRc01084				6.3E-41			
25352	ENU09147	ANI61C1097 8:1139..422			GTBX	AFUc10468				8E-37			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	Description
25353	ENU09148	ANI61C9302:1377..310			GTBX	"AFUc10685, AFUc15487"				"1.6e-66, 2.6e-15"			
25354	ENU09149	ANI61C9308:3085..3645			GTBX	"AFUc01566, AFUc02071"				"7.9e-38, 2.7e-18"			
25355	ENU09150	ANI61C10980:35..700			GTBX	AFUc04598				2.2E-28			
25356	ENU09151	ANI61C10981:7354..7898			GTBX	AFUc08664				2.4E-33			
25357	ENU09152	ANI61C10989:720..515			GTBX	AFUc12150				4.4E-39			
25358	ENU09153	ANI61C9317:662..250			GTBX	AFUc13330				1.5E-33			
25359	ENU09154	ANI61C9317:1109..2233			GTBX	"AFUc00802, AFUc20080, CALc06223"				"3.7e-48, 4.2e-14, 4.0e-19"			
25360	ENU09155	ANI61C9318:4746..5269			GTBX	"AFUc07003, AFUc07003, AFUc10141"				"6.6e-111, 7.7e-89, 6.1e-135"			
25361	ENU09156	ANI61C10991:621..883			GTBX	U00094				2.1e-49			
25362	ENU09157	ANI61C10997:8203..9278			GTBX	"AFUc12472, AFUc14082"				"2.4e-45, 3.0e-56"			
25363	ENU09158	ANI61C10999:4895..5915			GTBX	FGRc21400				1.6E-28			
25364	ENU09159	ANI61C9322:484..1044			GTBX	AFUc15756				6.7E-26			
25365	ENU09160	ANI61C9325:1369..280			GTBX	"AFUc11534, AFUc18844, CALc03970"				"8.0e-103, 1.6e-37, 5.1e-62"			

Gene annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25366	ENU09161	ANI61C8601: 282..17			GTBX	AFUc08235				4.1E-30			
25367	ENU09162	ANI61C9331: 1071..388			GTBX	AFUc13604				2.3E-35			
25368	ENU09163	ANI61C9332: 444..5			GTBX	"AFUc10065, FGRc19031"				"1.5e-30, 2.9e-12"			
25369	ENU09164	ANI61C8605: 420..208			GTBX	AFUc06416				5.3E-44			
25370	ENU09165	ANI61C9338: 2923..37			GTBX	"AFUc09246, AFUc11804, CALc06165, FGRc18522"				"3.8e-35, 2.2e-225, 2.0e-183, 6.1e-37"			
25371	ENU09166	ANI61C8612: 16..372			GTBX	AFUc09632				1.1E-45			
25372	ENU09167	ANI61C8612: 2351..879			GTBX	"AFUc06058, AFUc09335"				"7.6e-07, 3.0e-80"			
25373	ENU09168	ANI61C9342: 2713..2181			GTBX	AFUc08063				5.5E-104			
25374	ENU09169	ANI61C8614: 2981..15			GTBX	"AFUc15297, FGRc05338, FGRc25875"				"3.0e-73, 7.9e-24, 7.7e-11"			
25375	ENU09170	ANI61C9344: 4379..4882			GTBX	AFUc11946				4.1E-23			
25376	ENU09171	ANI61C8619: 3798..2506			GTBX	AFUc12001				8.5E-46			
25377	ENU09172	ANI61C8620: 1357..303			GTBX	"AFUc12034, CALc05986"				"2.6e-24, 3.2e-86"			
25378	ENU09173	ANI61C8620: 5794..6098			GTBX	AFUc14066				1.3E-110			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25379	ENU09174	ANI61C9355: 1253..680			GTBX	AFUc15687				9.2E-108			
25380	ENU09175	ANI61C8628: 36..656			GTBX	AFUc06137				2.8E-77			
25381	ENU09176	ANI61C9357: 137..1530			GTBX	AFUc09529				2.2E-49			
25382	ENU09177	ANI61C7900: 2532..4277			GTBX	"AFUc08848, AFUc09907, AFUc20452"				"7.5e-39, 2.4e-73, 1.6e-11"			
25383	ENU09178	ANI61C8631: 1103..2171			GTBX	AFUc19468				7.7E-45			
25384	ENU09179	ANI61C8631: 4111..2590			GTBX	"AFUc08405, AFUc16754, FGRC14352, Z71257"				"1.2e-107, 1.3e-33, 1.3e-37, 2.5e-81"			
25385	ENU09180	ANI61C9363: 2758..3087			GTBX	AFUc22414				1E-31			
25386	ENU09181	ANI61C8636: 895..300			GTBX	"AFUc01391, FGRC18380"				"3.0e-11, 2.2e-37"			
25387	ENU09182	ANI61C8638: 1064..405			GTBX	AFUc10092				1.3E-25			
25388	ENU09183	ANI61C9371: 1504..552			GTBX	AFUc12786				5.8E-50			
25389	ENU09184	ANI61C8645: 1124..1467			GTBX	AFUc11981				4.8E-31			
25390	ENU09185	ANI61C7918: 301..11			GTBX	AFUc01678				1.6E-27			
25391	ENU09186	ANI61C7918: 1104..1421			GTBX	AFUc14675				1.4E-28			

Sequence Definition

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25392	ENU09187	ANI61C9377: 493..810			GTBX	"AFUc12614, FGRc18368"				"1.5e-113, 2.6e-07" 1.5E-77			
25393	ENU09188	ANI61C9378: 906..1421			GTBX	AFUc11838							
25394	ENU09189	ANI61C8650: 3512..3901			GTBX	AFUc12134				2.5E-43			
25395	ENU09190	ANI61C7924: 412..8			GTBX	AFUc15732				2.7E-26			
25396	ENU09191	ANI61C8653: 1726..828			GTBX	AFUc13073				1.2E-130			
25397	ENU09192	ANI61C9383: 6530..7124			GTBX	AFUc17773				5.3E-67			
25398	ENU09193	ANI61C8656: 3851..3351			GTBX	AFUc05544				8.9E-73			
25399	ENU09194	ANI61C8657: 133..693			GTBX	AFUc08713				1.9E-58			
25400	ENU09195	ANI61C8659: 2496..3023			GTBX	"AFUc03782, FGRc10049"				"1.0e-18, 4.9e-38"			
25401	ENU09196	ANI61C7930: 659..1267			GTBX	"AFUc05717, AFUc21348"				"6.6e-43, 1.6e-09"			
25402	ENU09197	ANI61C8661: 3313..3669			GTBX	FGRc07994				1.6E-28			
25403	ENU09198	ANI61C8667: 78..575			GTBX	AFUc05732				5.1E-32			
25404	ENU09199	ANI61C9398: 391..77			GTBX	AFUc20294				1.1E-23			
25405	ENU09200	ANI61C7941: 923..25			GTBX	CALc05278				1.2E-32			

Geneious

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25406	ENU09201	ANI61C8670: 1370..185			GTBX	"FGRc08201, Y13135"				"1.0e-15, 4.4e-33"			
25407	ENU09202	ANI61C8675: 1001..198			GTBX	"AFUc00793, FGRc05104, FGRc16937"				"1.1e-42, 2.9e-13, 1.3e-27"			
25408	ENU09203	ANI61C7953: 1094..460			GTBX	"AFUc10606, AFUc21738"				"8.2e-37, 7.6e-63"			
25409	ENU09204	ANI61C8684: 649..89			GTBX	AFUc05878				5.6E-37			
25410	ENU09205	ANI61C8686: 4315..5067			GTBX	AFUc14227				1.5E-32			
25411	ENU09206	ANI61C8687: 2002..1217			GTBX	"AFUc18036, FGRc00673"				"5.6e-34, 1.9e-46"			
25412	ENU09207	ANI61C8694: 1591..479			GTBX	"AFUc08873, FGRc22249"				"6.3e-98, 1.0e-48"			
25413	ENU09208	ANI61C7976: 322..71			GTBX	AFUc18580				1.7E-30			
25414	ENU09209	ANI61C5001: 1403..1140			GTBX	"AFUc02640, Y13134"				"1.7e-30, 5.7e-119"			
25415	ENU09210	ANI61C5009: 24..377			GTBX	FGRc17279				4.8E-39			
25416	ENU09211	ANI61C7980: 53..1288			GTBX	AFUc11561				4.4E-51			
25417	ENU09212	ANI61C5019: 76..693			GTBX	AFUc08840				9.1E-56			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25418	ENU09213	ANI61C7995: 1601..6527			GTBX	"AFUc01564, AFUc05116, AFUc09051, AFUc11907, AFUc11907"				"1.9e-44, 1.1e-118, 1.5e-129, 2.7e-65, 7.2e-77"			
25419	ENU09214	ANI61C4300: 1696..1159			GTBX	"AFUc08580, CALc03532"				"5.0e-68, 1.7e-70"			
25420	ENU09215	ANI61C4303: 8..436			GTBX	AFUc03796				9.3E-47			
25421	ENU09216	ANI61C5033: 40..1000			GTBX	AFUc06232				3.8E-70			
25422	ENU09217	ANI61C5036: 600..238			GTBX	"AFUc14677, AFUc15942"				"3.5e-27, 5.0e-08"			
25423	ENU09218	ANI61C4307: 1506..298			GTBX	"AFUc03507, AFUc09984, AFUc12002"				"1.9e-46, 2.0e-41, 3.3e-09"			
25424	ENU09219	ANI61C5037: 994..581			GTBX	AFUc15029				6.6E-33			
25425	ENU09220	ANI61C4310: 1263..517			GTBX	AFUc13413				4.4E-144			
25426	ENU09221	ANI61C4314: 115..406			GTBX	AFUc14056				6.6E-29			
25427	ENU09222	ANI61C4317: 1103..288			GTBX	AFUc13039				1.8E-48			
25428	ENU09223	ANI61C4320: 616..2524			GTBX	AFUc12578				2.4E-249			
25429	ENU09224	ANI61S957:5 40..1			GTBX	AFUc13345				4.4E-34			
25430	ENU09225	ANI61C3603: 5..547			GTBX	AFUc12517				2.2E-39			

Genomic Data

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25431	ENU09226	ANI61C4336: 728..1			GTBX	AFUc15803				1.4E-40			
25432	ENU09227	ANI61C4337: 952..483			GTBX	"AFUc13626, FGRc03674"				"3.8e-48, 1.2e-40"			
25433	ENU09228	ANI61C4338: 666..96			GTBX	"AFUc13451, AFUc13451"				"1.7e-54, 1.7e-61"			
25434	ENU09229	ANI61C4341: 829..287			GTBX	AFUc01317				3.4E-35			
25435	ENU09230	ANI61C4344: 3049..1141			GTBX	"AFUc12501, CALc06236"				"2.4e-17, 1.1e-94"			
25436	ENU09231	ANI61C3616: 1216..1622			GTBX	AFUc11581				3.2E-33			
25437	ENU09232	ANI61C3617: 1144..657			GTBX	AFUc07024				6.9E-65			
25438	ENU09233	ANI61C3619: 755..48			GTBX	"AFUc12259, Y13138"				"3.9e-58, 1.8e-10"			
25439	ENU09234	ANI61C3621: 68..522			GTBX	CALc03177				3.4E-44			
25440	ENU09235	ANI61C3624: 887..140			GTBX	FGRc06045				4.9E-24			
25441	ENU09236	ANI61C3626: 905..3359			GTBX	"AFUc13163, AFUc13851"				"6.4e-96, 5.4e-119"			
25442	ENU09237	ANI61C5085: 1915..5			GTBX	"AFUc11103, D50617"				"2.3e-108, 1.2e-157"			
25443	ENU09238	ANI61C3627: 7636..8229			GTBX	"AFUc03814, AFUc21290"				"2.0e-37, 1.8e-12"			
25444	ENU09239	ANI61C4357: 3358..4103			GTBX	"AFUc13706, AFUc22334, FGRc07656"				"5.6e-33, 4.7e-38, 2.4e-29"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25445	ENU09240	ANI61C4358: 671..1564			GTBX	AFUc09818				2.3E-91			
25446	ENU09241	ANI61C4359: 163..1020			GTBX	AFUc08911				1.4E-42			
25447	ENU09242	ANI61C5089: 65..538			GTBX	AFUc00666				1.8E-48			
25448	ENU09243	ANI61S4199: 93..693			GTBX	AFUc15350				8E-41			
25449	ENU09244	ANI61C3636: 6447..7685			GTBX	AFUc20583				1.6E-24			
25450	ENU09245	ANI61C4365: 67..429			GTBX	AFUc10569				2.5E-29			
25451	ENU09246	ANI61C4368: 2709..1873			GTBX	AFUc11858				1.1E-108			
25452	ENU09247	ANI61C5097: 487..44			GTBX	AFUc05222				1.2E-24			
25453	ENU09248	ANI61S3472: 367..44			GTBX	"AFUc18364, CALc04995"				"7.5e-43, 3.5e-19"			
25454	ENU09249	ANI61C3640: 1580..893			GTBX	AFUc15969				3.1E-153			
25455	ENU09250	ANI61C4370: 216..1478			GTBX	"AFUc13516, AFUc14043, AFUc15051, FGRc01953"				"3.6e-42, 8.1e-24, 5.2e-105, 8.5e-21"			
25456	ENU09251	ANI61C2912: 629..16			GTBX	AFUc10688				9E-43			
25457	ENU09252	ANI61C4373: 445..695			GTBX	AFUc09914				9.6E-53			

Table 6: Contigs

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25458	ENU09253	ANI61C3645: 5320..6232			GTBX	FGRc09513				1.3E-21			
25459	ENU09254	ANI61C4378: 239..1305			GTBX	"AFUc02594, AFUc07825"				"2.6e-23, 4.9e-61"			
25460	ENU09255	ANI61S3489: 113..452			GTBX	CALc04906				9.1E-48			
25461	ENU09256	ANI61C2920: 965..1437			GTBX	Y13140				2.1e-24			
25462	ENU09257	ANI61C3650: 1816..3768			GTBX	AFUc15925				1.7E-151			
25463	ENU09258	ANI61C4382: 39..667			GTBX	AFUc06115				3.9E-28			
25464	ENU09259	ANI61C3655: 5..607			GTBX	"AFUc04082, FGRc03487"				"1.1e-16, 2.7e-26"			
25465	ENU09260	ANI61C2927: 556..311			GTBX	AFUc10442				7.5E-25			
25466	ENU09261	ANI61C2932: 377..873			GTBX	CALc04475				4.6E-79			
25467	ENU09262	ANI61C3661: 613..2			GTBX	"AFUc01462, AFUc19592"				"1.1e-31, 2.0e-18"			
25468	ENU09263	ANI61C4391: 2513..355			GTBX	"AFUc13024, AFUc15301"				"2.3e-68, 7.6e-132"			
25469	ENU09264	ANI61C4391: 5770..4632			GTBX	"AFUc08279, Y13139"				"1.2e-32, 5.3e-65"			
25470	ENU09265	ANI61C2934: 335..1188			GTBX	"AFUc11881, AFUc11881"				"1.7e-77, 2.7e-77"			
25471	ENU09266	ANI61C4392: 918..57			GTBX	AFUc07215				1.1E-54			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	Description
25486	ENU09281	ANI61C9439: 80..469			GTBX	AFUc15622				8.9E-30			
25487	ENU09282	ANI61C9440: 779..462			GTBX	AFUc11219				3.3E-61			
25488	ENU09283	ANI61C9440: 3473..3216			GTBX	AFUc08291				8.7E-44			
25489	ENU09284	ANI61C9441: 564..293			GTBX	AFUc08255				8.9E-26			
25490	ENU09285	ANI61C8713: 857..341			GTBX	AFUc05686				3.6E-29			
25491	ENU09286	ANI61C8714: 1347..1968			GTBX	AFUc20415				2E-24			
25492	ENU09287	ANI61C9445: 256..1691			GTBX	AFUc07629				5.2E-69			
25493	ENU09288	ANI61C9446: 221..547			GTBX	AFUc12171				4.8E-35			
25494	ENU09289	ANI61C9451: 4905..5724			GTBX	"AFUc05775, CALc05482"				"7.3e-64, 9.1e-41"			
25495	ENU09290	ANI61C8722: 765..153			GTBX	AFUc03370				5.4E-35			
25496	ENU09291	ANI61C8722: 2606..3753			GTBX	"AFUc03885, AFUc11035"				"1.8e-30, 3.8e-53"			
25497	ENU09292	ANI61C9455: 480..79			GTBX	AFUc18390				2.9E-23			
25498	ENU09293	ANI61C9456: 1440..613			GTBX	AFUc12641				1.1E-86			
25499	ENU09294	ANI61C8727: 4183..3316			GTBX	AFUc09501				1.1E-72			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25500	ENU09295	ANI61C9459: 759..1691			GTBX	"AFUc18002, AFUc20595"				"3.4e-58, 1.5e-39"			
25501	ENU09296	ANI61C8730: 4397..5083			GTBX	"AFUc07855, FGRc11749"				"1.1e-24, 1.7e-09"			
25502	ENU09297	ANI61C9461: 1997..2263			GTBX	AFUc03878				2.7E-36			
25503	ENU09298	ANI61C9464: 1019..1336			GTBX	AFUc10300				2.6E-29			
25504	ENU09299	ANI61C9465: 2884..3407			GTBX	"AFUc08665, AFUc08665"				"8.6e-122, 9.5e-97"			
25505	ENU09300	ANI61C8737: 1091..741			GTBX	AFUc12153				2.4E-35			
25506	ENU09301	ANI61C9469: 248..1142			GTBX	AFUc11644				8.5E-33			
25507	ENU09302	ANI61C8741: 856..1840			GTBX	AFUc13104				1.4E-61			
25508	ENU09303	ANI61C9470: 774..202			GTBX	AFUc15952				4.4E-72			
25509	ENU09304	ANI61C8743: 4032..4467			GTBX	AFUc15883				8.5E-24			
25510	ENU09305	ANI61C8745: 778..11			GTBX	AFUc07060				4E-35			
25511	ENU09306	ANI61C9477: 2962..3512			GTBX	AFUc09065				2E-58			
25512	ENU09307	ANI61C9479: 1230..7			GTBX	AFUc14503				1.5E-32			
25513	ENU09308	ANI61C8750: 1390..2176			GTBX	CALc06230				1.2E-262			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25528	ENU09323	ANI61C5110: 1141..410			GTBX	"AFUc18303, CALc06183"				"1.2e-34, 1.4e-90"			
25529	ENU09324	ANI61C5111: 912..1773			GTBX	"AFUc05704, AFUc13358"				"1.1e-34, 1.1e-34"			
25530	ENU09325	ANI61C5115: 1345..1022			GTBX	AFUc19450				1.1E-44			
25531	ENU09326	ANI61C5119: 582..14			GTBX	AFUc07458				2.7E-28			
25532	ENU09327	ANI61C5124: 804..1031			GTBX	AFUc07545				5.5E-22			
25533	ENU09328	ANI61C4400: 2306..1797			GTBX	"FGRc08787, FGRc14740"				"7.0e-21, 4.4e-17"			
25534	ENU09329	ANI61C4401: 2345..1654			GTBX	"AFUc05876, FGRc05155"				"4.8e-30, 7.0e-10"			
25535	ENU09330	ANI61C4406: 538..251			GTBX	AFUc07366				1.4E-21			
25536	ENU09331	ANI61C4407: 4154..5342			GTBX	"AFUc01633, AFUc19340"				"6.1e-20, 1.6e-39"			
25537	ENU09332	ANI61C4408: 1390..3			GTBX	AFUc13334				8E-99			
25538	ENU09333	ANI61C5137: 1034..13			GTBX	U00091				3.4e-45			
25539	ENU09334	ANI61C4409: 579..2167			GTBX	"AFUc02131, CALc04637, FGRc10200"				"1.1e-80, 4.6e-17, 7.3e-65"			
25540	ENU09335	ANI61S4243: 78..437			GTBX	Y18138				2.5e-15			
25541	ENU09336	ANI61S3519: 56..256			GTBX	AFUc13413				4E-24			

Contig with

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25542	ENU09337	ANI61C5143: 665..148			GTBX	AFUc22527				2.5E-69			
25543	ENU09338	ANI61C4415: 697..308			GTBX	AFUc08588				8.1E-50			
25544	ENU09339	ANI61C4415: 1944..2984			GTBX	"AFUc14631, Z71256"				"5.7e-117, 4.2e-40"			
25545	ENU09340	ANI61C5153: 400..1153			GTBX	AFUc15665				9.9E-110			
25546	ENU09341	ANI61C4428: 2186..509			GTBX	"AFUc03693, AFUc15500"				"1.3e-09, 4.9e-36"			
25547	ENU09342	ANI61C4429: 456..989			GTBX	AFUc02454				1.9E-48			
25548	ENU09343	ANI61C4430: 590..6			GTBX	"AFUc05777, AFUc11518"				"3.2e-11, 3.9e-35"			
25549	ENU09344	ANI61C4431: 865..1682			GTBX	CALc05985				7.5E-34			
25550	ENU09345	ANI61C4431: 2288..1929			GTBX	AFUc19720				1.9E-32			
25551	ENU09346	ANI61C5161: 6479..8758			GTBX	"AFUc15497, FGRc01538"				"2.1e-195, 1.2e-29"			
25552	ENU09347	ANI61C4435: 44..619			GTBX	AFUc10109				2.3E-49			
25553	ENU09348	ANI61C4436: 562..5			GTBX	"AFUc20304, FGRc08260"				"2.3e-42, 1.2e-10"			
25554	ENU09349	ANI61C4439: 603..957			GTBX	"AFUc15143, AFUc22336"				"4.2e-45, 1.0e-09"			
25555	ENU09350	ANI61C3716: 495..52			GTBX	AFUc17201				8.4E-27			

Sequence Alignment

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	Description
25556	ENU09351	ANI61C5184: 1185..739			GTBX	FGRc06929				2.5E-27			
25557	ENU09352	ANI61C5184: 1958..2668			GTBX	"AFUc02805, AFUc21089"				"2.8e-37, 4.9e-21"			
25558	ENU09353	ANI61C5189: 1018..77			GTBX	AFUc11900				1.1E-105			
25559	ENU09354	ANI61C3732: 61..673			GTBX	AFUc01401				2.1E-67			
25560	ENU09355	ANI61C3733: 3210..1934			GTBX	"FGRc03487, FGRc09159"				"5.7e-40, 2.8e-32"			
25561	ENU09356	ANI61C5191: 8..424			GTBX	AFUc09001				5.6E-37			
25562	ENU09357	ANI61C3738: 6..715			GTBX	"AFUc03774, AFUc13364"				"8.2e-10, 1.8e-39"			
25563	ENU09358	ANI61C5199: 1578..1127			GTBX	AFUc14538				3.3E-24			
25564	ENU09359	ANI61S2843: 428..10			GTBX	"AFUc14444, FGRc10441"				"8.6e-31, 9.2e-07"			
25565	ENU09360	ANI61C3747: 51..467			GTBX	AFUc14515				1.4E-45			
25566	ENU09361	ANI61S3584: 97..486			GTBX	AFUc10638				2.5E-31			
25567	ENU09362	ANI61C3751: 892..219			GTBX	FGRc00730				4.1E-26			
25568	ENU09363	ANI61C3754: 4387..4890			GTBX	"AFUc02406, CALc04204"				"8.0e-11, 5.7e-83"			
25569	ENU09364	ANI61C4484: 195..646			GTBX	AFUc11050				2.8E-26			

GenBank accession

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25570	ENU09365	ANI61C4485: 470..1338			GTBX	AFUc11852				2.8E-121			
25571	ENU09366	ANI61C3758: 368..568			GTBX	FGRc26076				1E-32			
25572	ENU09367	ANI61S2863: 456..103			GTBX	AFUc00783				2E-55			
25573	ENU09368	ANI61C4495: 836..438			GTBX	AFUc01513				6.8E-93			
25574	ENU09369	ANI61C4496: 973..1308			GTBX	FGRc10958				4E-67			
25575	ENU09370	ANI61C4497: 1059..277			GTBX	AFUc15397				2.5E-74			
25576	ENU09371	ANI61C3777: 414..651			GTBX	"AFUc21795, FGRc13545"				"1.3e-28, 3.1e-25"			
25577	ENU09372	ANI61C3785: 1070..87			GTBX	"AFUc09448, FGRc15416"				"3.1e-107, 8.7e-28"			
25578	ENU09373	ANI61C3786: 347..670			GTBX	AFUc15598				4.3E-84			
25579	ENU09374	ANI61C9504: 1509..983			GTBX	AFUc15752				6E-62			
25580	ENU09375	ANI61C9505: 6..593			GTBX	FGRc08493				8.8E-24			
25581	ENU09376	ANI61C9508: 1395..319			GTBX	"AFUc02590, AFUc21220"				"1.3e-22, 3.5e-14"			
25582	ENU09377	ANI61C9521: 1526..810			GTBX	"AFUc02035, FGRc16341"				"5.7e-54, 1.2e-07"			
25583	ENU09378	ANI61C9523: 2194..13			GTBX	"AFUc08207, AFUc09870"				"1.8e-65, 7.3e-119"			

GeneWise2 Gene Annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25584	ENU09379	ANI61C9524: 491..986			GTBX	AFUc15203				2.5E-28			
25585	ENU09380	ANI61C9528: 1204..737			GTBX	AFUc05005				1.1E-24			
25586	ENU09381	ANI61C9529: 368..93			GTBX	AFUc05865				5.5E-26			
25587	ENU09382	ANI61C9531: 724..2			GTBX	AFUc08448				6.3E-38			
25588	ENU09383	ANI61C8803: 60..1376			GTBX	"AFUc06649, AFUc09276, AFUc09645, AFUc15313, FGRC11399"				"8.5e-10, 8.2e-10, 6.1e-38, 3.1e-53, 5.2e-08" 2.6E-64			
25589	ENU09384	ANI61C8808: 3412..4903			GTBX	FGRC04144							
25590	ENU09385	ANI61C8809: 304..1298			GTBX	"AFUc10278, FGRC24365"				"1.3e-76, 1.7e-38"			
25591	ENU09386	ANI61C9539: 1484..1182			GTBX	AFUc03644				3.4E-48			
25592	ENU09387	ANI61C8814: 3867..5544			GTBX	AFUc12826				4.6E-78			
25593	ENU09388	ANI61C9543: 28..687			GTBX	"AFUc05060, AFUc19153"				"5.8e-10, 7.8e-22"			
25594	ENU09389	ANI61C8815: 226..648			GTBX	AFUc22266				2.3E-27			
25595	ENU09390	ANI61C8818: 1872..1054			GTBX	AFUc13384				9.4E-45			
25596	ENU09391	ANI61C9547: 556..56			GTBX	AFUc09688				6.5E-47			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25597	ENU09392	ANI61C9548:1206..482			GTBX	AFUc02615				5E-21			
25598	ENU09393	ANI61C9549:160..864			GTBX	AFUc01363				2.1E-25			
25599	ENU09394	ANI61C8820:2367..49			GTBX	"AFUc00774, AFUc02877, AFUc05794, AFUc15944, AFUc22301" AFUc10083				"8.7e-55, 1.1e-11, 3.2e-60, 6.1e-25, 3.4e-16" 7.2E-44			
25600	ENU09395	ANI61C8821:1333..384			GTBX								
25601	ENU09396	ANI61C8821:1619..2665			GTBX	"FGRc04178, Z71256"				"5.1e-08, 6.6e-88"			
25602	ENU09397	ANI61C9553:2145..406			GTBX	"AFUc06513, AFUc07337, CALc06139"				"1.2e-55, 9.6e-62, 4.0e-40" 2.8E-61			
25603	ENU09398	ANI61C9556:7313..7830			GTBX	FGRc11417							
25604	ENU09399	ANI61C8827:1639..428			GTBX	FGRc06586				7.5E-35			
25605	ENU09400	ANI61C8831:2299..2823			GTBX	"AFUc01894, CALc05378"				"4.2e-36, 1.8e-38"			
25606	ENU09401	ANI61C9566:2382..1796			GTBX	"AFUc14024, FGRc03629"				"8.2e-20, 5.8e-27" 2.6E-28			
25607	ENU09402	ANI61C9567:1721..2586			GTBX	AFUc08775							
25608	ENU09403	ANI61C9569:1936..900			GTBX	"AFUc11045, FGRc07076"				"1.3e-26, 2.2e-09" 4.9E-122			
25609	ENU09404	ANI61C9572:3019..2194			GTBX	CALc05999							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25610	ENU09405	ANI61C8846: 2..490			GTBX	AFUc09502				2.1E-50			
25611	ENU09406	ANI61C9579: 4150..3347			GTBX	AFUc05155				2.4E-30			
25612	ENU09407	ANI61C9582: 1668..221			GTBX	"AFUc09791, AFUc14294, AFUc15490"				"1.2e-28, 3.4e-45, 5.5e-78"			
25613	ENU09408	ANI61C8854: 633..1820			GTBX	"AFUc03263, AFUc08210"				"1.4e-07, 1.2e-33"			
25614	ENU09409	ANI61C8857: 2334..2536			GTBX	AFUc06435				1.5E-121			
25615	ENU09410	ANI61C9592: 105..520			GTBX	"FGRc09345, FGRc21977"				"6.9e-29, 2.9e-14"			
25616	ENU09411	ANI61C9595: 1129..674			GTBX	AFUc14898				6.6E-58			
25617	ENU09412	ANI61C8867: 803..26			GTBX	"AFUc08398, CALc05816"				"5.9e-24, 1.3e-17"			
25618	ENU09413	ANI61C8873: 8152..7032			GTBX	AFUc12824				2.7E-89			
25619	ENU09414	ANI61C8875: 12..1277			GTBX	AFUc14483				4.9E-162			
25620	ENU09415	ANI61C8878: 44..934			GTBX	AFUc14882				7.3E-46			
25621	ENU09416	ANI61C8879: 1404..2768			GTBX	AFUc14241				1.9E-70			
25622	ENU09417	ANI61C8884: 1067..53			GTBX	AFUc07086				4.5E-95			
25623	ENU09418	ANI61C8888: 1156..1536			GTBX	U00093				1.2e-74			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25624	ENU09419	ANI61C8889: 702..1898			GTBX	"AFUc03016, CALc03652"				"1.4e-55, 2.8e-59"			
25625	ENU09420	ANI61C8892: 1683..192			GTBX	"AFUc13932, FGRc11747, FGRc17309, FGRc26009"				"1.4e-25, 1.3e-10, 5.3e-09, 1.1e-16"			
25626	ENU09421	ANI61C8895: 67..904			GTBX	"AFUc11204, AFUc11814"				"2.5e-34, 1.2e-104"			
25627	ENU09422	ANI61C5207: 316..663			GTBX	AFUc15608				1.5E-46			
25628	ENU09423	ANI61C5207: 1872..793			GTBX	"AFUc03870, AFUc07633, AFUc19031"				"6.3e-16, 1.2e-19, 9.9e-70"			
25629	ENU09424	ANI61C5208: 2536..2216			GTBX	"AFUc06181, Y13138"				"1.5e-32, 9.0e-162"			
25630	ENU09425	ANI61C5209: 1457..2136			GTBX	"AFUc17725, FGRc11373"				"3.9e-27, 7.4e-19"			
25631	ENU09426	ANI61C5210: 2139..105			GTBX	AFUc15196				3.7E-186			
25632	ENU09427	ANI61C5215: 2509..2763			GTBX	AFUc15348				7.2E-121			
25633	ENU09428	ANI61C5222: 2322..719			GTBX	"AFUc07927, FGRc02874"				"7.9e-86, 9.0e-10"			
25634	ENU09429	ANI61C5224: 1472..13			GTBX	CALc05716				1.7E-119			
25635	ENU09430	ANI61C5228: 399..962			GTBX	AFUc14750				1.2E-90			
25636	ENU09431	ANI61S3608: 177..573			GTBX	AFUc22203				1.8E-23			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25637	ENU09432	ANI61C4506: 499..29			GTBX	AFUc15788				9.6E-33			
25638	ENU09433	ANI61C5237: 420..1271			GTBX	AFUc14942				6.9E-104			
25639	ENU09434	ANI61C5247: 4110..4852			GTBX	AFUc13730				1E-97			
25640	ENU09435	ANI61C4519: 2052..587			GTBX	AFUc15419				5.4E-127			
25641	ENU09436	ANI61C5251: 672..47			GTBX	Y13137				4.1e-43			
25642	ENU09437	ANI61C4526: 1413..1054			GTBX	AFUc15744				1.3E-147			
25643	ENU09438	ANI61C5256: 674..26			GTBX	"AFUc06812, AFUc08626"				"1.7e-44, 2.8e-09"			
25644	ENU09439	ANI61C4528: 509..147			GTBX	AFUc15759				1.9E-29			
25645	ENU09440	ANI61S4368: 60..639			GTBX	AFUc07754				2.2E-21			
25646	ENU09441	ANI61C3803: 1096..2			GTBX	"AFUc08591, AFUc13887"				"1.1e-55, 4.4e-75"			
25647	ENU09442	ANI61C3805: 4035..3580			GTBX	AFUc04676				6.3E-45			
25648	ENU09443	ANI61C3808: 743..411			GTBX	Y13138				5.8e-14			
25649	ENU09444	ANI61C5269: 1394..2229			GTBX	"AFUc02280, AFUc22008"				"9.4e-57, 2.0e-43"			
25650	ENU09445	ANI61C3810: 82..437			GTBX	AFUc15201				4E-52			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25651	ENU09446	ANI61C3811: 1376..1654			GTBX	AFUc06467				3.5E-30			
25652	ENU09447	ANI61C4542: 916..574			GTBX	"AFUc02869, AFUc02869"				"1.7e-65, 4.7e-26"			
25653	ENU09448	ANI61C3813: 1846..3158			GTBX	"FGRc12841, FGRc22473, FGRc23239"				"4.6e-26, 7.9e-35, 1.6e-43"			
25654	ENU09449	ANI61C5273: 2..1156			GTBX	"AFUc05117, AFUc11543"				"5.4e-27, 1.6e-92"			
25655	ENU09450	ANI61C3817: 78..1162			GTBX	AFUc12851				2.7E-75			
25656	ENU09451	ANI61C3821: 672..411			GTBX	AFUc15435				4.7E-56			
25657	ENU09452	ANI61C4551: 151..475			GTBX	AFUc18864				3.2E-45			
25658	ENU09453	ANI61C5280: 1840..2502			GTBX	"AFUc04510, AFUc18595"				"1.2e-24, 2.7e-07"			
25659	ENU09454	ANI61C3823: 22..252			GTBX	AFUc12507				7.4E-60			
25660	ENU09455	ANI61C3824: 595..981			GTBX	FGRc23435				2.8E-21			
25661	ENU09456	ANI61C3825: 375..735			GTBX	"AFUc06063, CALc02020, Y13134"				"5.9e-40, 3.0e-16, 6.7e-17"			
25662	ENU09457	ANI61C5283: 954..108			GTBX	AFUc12676				4.8E-36			
25663	ENU09458	ANI61C5286: 531..786			GTBX	"AFUc12628, AFUc12628, FGRc07656"				"5.6e-24, 6.7e-29, 3.4e-13"			
25664	ENU09459	ANI61C4559: 151..684			GTBX	AFUc21004				3.4E-31			

Gene Description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25665	ENU09460	ANI61S4392: 18..500			GTBX	"AFUc01686, Y13138"				"1.1e-43, 2.9e-62"			
25666	ENU09461	ANI61C4561: 27..754			GTBX	"AFUc10269, FGRc22925"				"3.0e-23, 2.5e-28"			
25667	ENU09462	ANI61C3833: 646..232			GTBX	FGRc04710				8.2E-72			
25668	ENU09463	ANI61C3834: 1167..1727			GTBX	AFUc16457				3.3E-29			
25669	ENU09464	ANI61C5294: 1041..654			GTBX	"AFUc15936, FGRc11101"				"1.2e-123, 5.2e-24"			
25670	ENU09465	ANI61S3674: 270..8			GTBX	AFUc10670				8.6E-33			
25671	ENU09466	ANI61C3840: 162..656			GTBX	"AFUc18322, AFUc21010"				"1.7e-19, 2.1e-26"			
25672	ENU09467	ANI61C4570: 2285..3385			GTBX	AFUc17804				1.3E-21			
25673	ENU09468	ANI61C4585: 983..30			GTBX	Y13135				4.5e-64			
25674	ENU09469	ANI61C4589: 727..290			GTBX	AFUc21610				2E-25			
25675	ENU09470	ANI61C3869: 25..390			GTBX	AFUc08072				4.6E-43			
25676	ENU09471	ANI61C4599: 54..440			GTBX	AFUc08426				1.4E-25			
25677	ENU09472	ANI61C3870: 791..270			GTBX	CALc05830				2.9E-34			
25678	ENU09473	ANI61C3877: 1384..1001			GTBX	AFUc01915				1.9E-47			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25679	ENU09474	ANI61C3878: 1289..596			GTBX	"CALc04339, FGRc02339"				"4.4e-76, 3.3e-84"			
25680	ENU09475	ANI61C3879: 684..79			GTBX	AFUc09507				2.3E-40			
25681	ENU09476	ANI61C3881: 785..207			GTBX	CALc03328				5.8E-44			
25682	ENU09477	ANI61C3888: 813..247			GTBX	AFUc05510				6.2E-28			
25683	ENU09478	ANI61C3889: 1158..606			GTBX	AFUc13973				9.9E-73			
25684	ENU09479	ANI61C3893: 1373..3			GTBX	"AFUc04394, AFUc14651"				"8.1e-41, 2.6e-96"			
25685	ENU09480	ANI61C3895: 540..755			GTBX	AFUc12362				1.1E-54			
25686	ENU09481	ANI61C9601: 7148..7954			GTBX	AFUc17920				5.3E-44			
25687	ENU09482	ANI61C9605: 1032..50			GTBX	AFUc12404				5.5E-76			
25688	ENU09483	ANI61C9609: 1184..573			GTBX	"AFUc12674, AFUc16179, FGRc06836"				"7.5e-22, 5.1e-25, 3.7e-61"			
25689	ENU09484	ANI61C9611: 1087..208			GTBX	CALc04433				2.7E-99			
25690	ENU09485	ANI61C9621: 2017..1559			GTBX	AFUc01710				9.7E-47			
25691	ENU09486	ANI61C9624: 1287..1999			GTBX	"AFUc04270, AFUc04681, AFUc04681"				"2.7e-49, 1.4e-28, 2.4e-35"			
25692	ENU09487	ANI61C8901: 1882..2697			GTBX	AFUc13517				4.7E-78			

[illegible]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25706	ENU09501	ANI61C9669: 3783..5102			GTBX	"AFUc10037, AFUc12096"				"1.4e-95, 5.2e-40"			
25707	ENU09502	ANI61C8941: 564..836			GTBX	AFUc07937				1.5E-56			
25708	ENU09503	ANI61C9675: 2597..749			GTBX	"AFUc10109, AFUc17198, AFUc17198, FGRe15837, FGRe26158"				"3.0e-78, 4.0e-21, 5.3e-23, 1.5e-21, 3.5e-13"			
25709	ENU09504	ANI61C9677: 2010..1543			GTBX	AFUc12413				1.7E-102			
25710	ENU09505	ANI61C8954: 683..447			GTBX	AFUc08873				6.9E-34			
25711	ENU09506	ANI61C9687: 829..2			GTBX	"FGRe12006, Y13136"				"1.2e-51, 5.3e-40"			
25712	ENU09507	ANI61C9691: 2115..1211			GTBX	AFUc05215				5.3E-41			
25713	ENU09508	ANI61C9692: 1160..606			GTBX	AFUc16896				2.9E-28			
25714	ENU09509	ANI61C9694: 4490..3594			GTBX	"AFUc20993, U00092"				"2.6e-46, 3.6e-07"			
25715	ENU09510	ANI61C8966: 5753..6363			GTBX	"AFUc06989, Z71256"				"4.3e-36, 4.6e-11"			
25716	ENU09511	ANI61C9695: 923..72			GTBX	"AFUc14005, AFUc20315"				"7.8e-29, 3.3e-73"			
25717	ENU09512	ANI61C8967: 2826..2269			GTBX	AFUc03802				4.7E-40			
25718	ENU09513	ANI61C8971: 1468..733			GTBX	"CALc05073, FGRe02949"				"1.2e-22, 7.5e-24"			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25719	ENU09514	ANI61C8973: 574..1417			GTBX	AFUc21866				1.9E-30			
25720	ENU09515	ANI61C8979: 129..506			GTBX	AFUc00391				5.9E-29			
25721	ENU09516	ANI61C8979: 3411..3851			GTBX	AFUc05896				9.6E-24			
25722	ENU09517	ANI61C6002: 1830..1440			GTBX	AFUc13365				4.5E-61			
25723	ENU09518	ANI61C6003: 1016..1437			GTBX	AFUc14299				3.9E-71			
25724	ENU09519	ANI61C8982: 756..2038			GTBX	"AFUc09202, Y13139"				"6.1e-92, 1.1e-28"			
25725	ENU09520	ANI61C8987: 5718..5065			GTBX	FGRc14942				2.8E-33			
25726	ENU09521	ANI61C8988: 29..1003			GTBX	"AFUc09518, FGRc00963"				"4.6e-37, 8.8e-14"			
25727	ENU09522	ANI61C6010: 705..413			GTBX	AFUc11775				3.6E-69			
25728	ENU09523	ANI61C8992: 1060..1268			GTBX	AFUc15788				6.5E-46			
25729	ENU09524	ANI61C6023: 22..959			GTBX	AFUc08361				2.1E-105			
25730	ENU09525	ANI61C6028: 698..112			GTBX	AFUc15445				2.8E-45			
25731	ENU09526	ANI61C5302: 804..1978			GTBX	"AFUc03529, FGRc15568, FGRc23030"				"3.9e-75, 1.9e-31, 6.8e-27"			
25732	ENU09527	ANI61C6032: 121..656			GTBX	FGRc24538				5.3E-24			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	% Description
25733	ENU09528	ANI61C5304: 20..1813			GTBX	"CALc04320, CALc06192"				"4.1e-46, 1.3e-114"			
25734	ENU09529	ANI61C5307: 1011..634			GTBX	AFUc13255				1.7E-36			
25735	ENU09530	ANI61C6040: 498..238			GTBX	AFUc14608				1.3E-22			
25736	ENU09531	ANI61C5312: 17..463			GTBX	AFUc08453				1.5E-54			
25737	ENU09532	ANI61C6044: 827..423			GTBX	"AFUc20402, CALc05987, FGRc05827"				"1.4e-19, 7.9e-53, 3.2e-52"			
25738	ENU09533	ANI61C5317: 3..599			GTBX	"AFUc20512, CALc05290"				"3.1e-46, 1.8e-07"			
25739	ENU09534	ANI61C5320: 383..24			GTBX	CALc05007				6.7E-28			
25740	ENU09535	ANI61C5322: 2464..874			GTBX	"AFUc11807, FGRc09518"				"4.3e-88, 4.4e-20"			
25741	ENU09536	ANI61C5323: 557..1220			GTBX	AFUc08478				9.2E-73			
25742	ENU09537	ANI61C6052: 840..342			GTBX	AFUc01410				9.1E-40			
25743	ENU09538	ANI61C5324: 1547..58			GTBX	"AFUc06920, AFUc07230, AFUc14567, Y13135"				"5.1e-54, 1.9e-34, 7.7e-11, 5.1e-13"			
25744	ENU09539	ANI61C6062: 377..39			GTBX	AFUc13039				3.2E-30			
25745	ENU09540	ANI61C4610: 78..674			GTBX	AFUc07396				4.1E-82			
25746	ENU09541	ANI61C5341: 1441..35			GTBX	"AFUc21842, CALc05774"				"8.4e-62, 1.9e-72"			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	% Description
25747	ENU09542	ANI61C6074:1430..126			GTBX	Y13137				7.4e-89			
25748	ENU09543	ANI61C5348:2041..49			GTBX	"AFUc04409, AFUc14023"				"2.3e-18, 2.3e-22"			
25749	ENU09544	ANI61C5351:3706..2627			GTBX	FGRc11453				1.5E-44			
25750	ENU09545	ANI61C5355:400..77			GTBX	AFUc22404				5.3E-47			
25751	ENU09546	ANI61C5363:1986..2330			GTBX	AFUc02673				1.1E-35			
25752	ENU09547	ANI61S3748:25..508			GTBX	AFUc19745				4.5E-46			
25753	ENU09548	ANI61C3914:1..336			GTBX	AFUc12813				2E-30			
25754	ENU09549	ANI61C5372:2782..3320			GTBX	AFUc10825				3E-56			
25755	ENU09550	ANI61C4644:385..122			GTBX	"AFUc14213, CALc06077"				"1.0e-23, 6.0e-13"			
25756	ENU09551	ANI61C3915:1063..782			GTBX	AFUc00550				1.3E-42			
25757	ENU09552	ANI61C5373:6..1136			GTBX	AFUc08943				2.9E-89			
25758	ENU09553	ANI61C5376:55..480			GTBX	AFUc05917				7.3E-30			
25759	ENU09554	ANI61C3920:2247..56			GTBX	"AFUc17196, AFUc18488, AFUc18488, FGRc00704, Y13134"				"1.3e-71, 3.5e-44, 3.5e-75, 2.7e-29, 1.3e-68"			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	Description
25760	ENU09555	ANI61C4650:1372..2			GTBX	"AFUc14849, FGRc00854"				"3.1e-10, 6.0e-32"			
25761	ENU09556	ANI61C4651:870..50			GTBX	"AFUc22660, FGRc07303"				"6.5e-29, 3.2e-52"			
25762	ENU09557	ANI61C4652:752..2207			GTBX	AFUc14076				8.4E-46			
25763	ENU09558	ANI61C5381:1004..492			GTBX	AFUc03475				4.2E-51			
25764	ENU09559	ANI61C3925:218..802			GTBX	AFUc15140				9.4E-57			
25765	ENU09560	ANI61C5385:1551..1769			GTBX	AFUc07950				2.4E-42			
25766	ENU09561	ANI61C4657:4223..6270			GTBX	"AFUc11820, AFUc12573, AFUc14610, Y13135"				"5.1e-145, 4.5e-84, 1.4e-15, 2.0e-98"			
25767	ENU09562	ANI61C3929:514..28			GTBX	AFUc01963				1.3E-45			
25768	ENU09563	ANI61C5387:1209..723			GTBX	FGRc03431				5.6E-46			
25769	ENU09564	ANI61C4659:1012..1228			GTBX	AFUc14550				3.7E-25			
25770	ENU09565	ANI61C5388:2432..2081			GTBX	"AFUc11974, AFUc14576"				"3.6e-40, 2.4e-67"			
25771	ENU09566	ANI61C5389:97..686			GTBX	AFUc10526				1.7E-51			
25772	ENU09567	ANI61C4663:149..637			GTBX	AFUc14674				1.6E-25			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25773	ENU09568	ANI61C5396:1207..3398			GTBX	"AFUc05105, AFUc11030, FGRc07318"				"1.0e-81, 2.1e-79, 3.6e-124"			
25774	ENU09569	ANI61C4667:422..34			GTBX	FGRc10474				2.6E-26			
25775	ENU09570	ANI61C4669:6..968			GTBX	"AFUc09487, FGRc08263"				"2.3e-103, 3.5e-33"			
25776	ENU09571	ANI61C5399:1944..519			GTBX	AFUc15972				5.6E-33			
25777	ENU09572	ANI61C4672:742..473			GTBX	AFUc13983				3.2E-32			
25778	ENU09573	ANI61C3953:2205..895			GTBX	"AFUc00630, AFUc16315"				"2.5e-36, 8.9e-30"			
25779	ENU09574	ANI61C4683:435..36			GTBX	AFUc11129				3.4E-35			
25780	ENU09575	ANI61C3956:1317..362			GTBX	"AFUc15086, Y13138"				"6.9e-43, 3.0e-21"			
25781	ENU09576	ANI61C3965:2616..2940			GTBX	AFUc14919				3.5E-65			
25782	ENU09577	ANI61C3966:924..1			GTBX	"AFUc19250, Y13138"				"1.7e-18, 1.8e-36"			
25783	ENU09578	ANI61C4698:651..1923			GTBX	"AFUc13453, FGRc11821"				"2.6e-83, 2.5e-47"			
25784	ENU09579	ANI61C3971:1048..34			GTBX	"AFUc00727, AFUc21727"				"1.9e-90, 5.3e-42"			
25785	ENU09580	ANI61C3972:3639..2620			GTBX	"AFUc02588, AFUc02588"				"8.1e-28, 9.6e-37"			
25786	ENU09581	ANI61C3973:2117..461			GTBX	"AFUc19352, CALc06116"				"6.3e-14, 7.6e-171"			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	Description
25787	ENU09582	ANI61C3977: 1953..643			GTBX	AFUc15344				2.9E-166			
25788	ENU09583	ANI61C3978: 843..82			GTBX	FGRc04709				6.4E-34			
25789	ENU09584	ANI61C1002: 2611..2219			GTBX	AFUc08610				1.1E-28			
25790	ENU09585	ANI61C1003: 2507..993			GTBX	"AFUc01633, AFUc19340, FGRc18569"				"1.9e-51, 1.4e-46, 1.6e-11"			
25791	ENU09586	ANI61C1014: 740..199			GTBX	AFUc02769				2E-26			
25792	ENU09587	ANI61C3992: 282..521			GTBX	AFUc20274				1.7E-29			
25793	ENU09588	ANI61C3995: 44..766			GTBX	"AFUc05280, AFUc21291"				"2.0e-14, 1.2e-43"			
25794	ENU09589	ANI61C1022: 766..454			GTBX	AFUc14424				2.6E-31			
25795	ENU09590	ANI61C1025: 556..32			GTBX	AFUc14916				7.3E-108			
25796	ENU09591	ANI61C1030: 3757..3323			GTBX	AFUc10051				9.9E-36			
25797	ENU09592	ANI61C1038: 712..1006			GTBX	"AFUc14099, FGRc00303"				"5.0e-52, 1.3e-12"			
25798	ENU09593	ANI61C1044: 1903..35			GTBX	AFUc08909				5.9E-121			
25799	ENU09594	ANI61C1052: 1095..102			GTBX	"AFUc03916, AFUc06334"				"2.8e-32, 5.4e-26"			
25800	ENU09595	ANI61C1053: 618..115			GTBX	AFUc12163				8.2E-69			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25801	ENU09596	ANI61C1056: 1..606			GTBX	"AFUc17783, CALc05720"				"7.4e-44, 8.3e-23"			
25802	ENU09597	ANI61C1058: 2606..2340			GTBX	AFUc12718				4.7E-23			
25803	ENU09598	ANI61C1069: 4950..5330			GTBX	AFUc15622				1.1E-58			
25804	ENU09599	ANI61C9702: 2851..385			GTBX	"AFUc18380, CALc02515, U00092"				"8.9e-49, 7.3e-93, 1.5e-284"			
25805	ENU09600	ANI61C9702: 4461..4919			GTBX	AFUc10199				1.4E-80			
25806	ENU09601	ANI61C9706: 4861..6696			GTBX	"CALc05544, Y13137"				"3.8e-234, 3.7e-307"			
25807	ENU09602	ANI61C9717: 419..1280			GTBX	"AFUc05673, AFUc07215"				"1.5e-31, 4.4e-123"			
25808	ENU09603	ANI61C9718: 618..277			GTBX	AFUc18240				3E-31			
25809	ENU09604	ANI61C1084: 317..835			GTBX	AFUc14920				1.2E-23			
25810	ENU09605	ANI61C9720: 356..1467			GTBX	"AFUc12550, CALc05628"				"3.7e-168, 1.6e-21"			
25811	ENU09606	ANI61C1095: 4166..4419			GTBX	"AFUc03966, FGRC09117"				"2.2e-32, 1.5e-10"			
25812	ENU09607	ANI61C9733: 2309..2918			GTBX	AFUc14559				2.3E-43			
25813	ENU09608	ANI61C9738: 3327..3604			GTBX	AFUc06208				4.3E-24			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25814	ENU09609	ANI61C9739: 7440..7764			GTBX	AFUc20780				3E-49			
25815	ENU09610	ANI61C9743: 1418..873			GTBX	"CALc05775, FGRc05013"				"2.8e-60, 1.9e-26"			
25816	ENU09611	ANI61C9752: 1283..51			GTBX	"AFUc14599, CALc02009"				"8.4e-132, 1.9e-07"			
25817	ENU09612	ANI61C9760: 3667..4155			GTBX	AFUc07682				1.8E-31			
25818	ENU09613	ANI61C9760: 5872..4366			GTBX	"AFUc07479, Y13134"				"2.6e-66, 1.2e-55"			
25819	ENU09614	ANI61C9769: 120..994			GTBX	AFUc07018				5.2E-44			
25820	ENU09615	ANI61C9773: 1037..200			GTBX	"AFUc08480, FGRc23544"				"3.2e-16, 1.7e-34"			
25821	ENU09616	ANI61C9775: 1364..2760			GTBX	"AFUc06544, AFUc15485"				"3.2e-35, 6.5e-73"			
25822	ENU09617	ANI61C9790: 415..3897			GTBX	"AFUc02169, AFUc12397, CALc01597, CALc04669"				"2.0e-70, 2.3e-252, 5.0e-19, 9.6e-114"			
25823	ENU09618	ANI61C9792: 540..156			GTBX	AFUc09788				5.2E-45			
25824	ENU09619	ANI61C9794: 3349..2897			GTBX	AFUc09569				1.8E-27			
25825	ENU09620	ANI61C6100: 325..100			GTBX	AFUc06484				2.5E-26			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25826	ENU09621	ANI61C6108: 208..1945			GTBX	"AFUc10825, AFUc14691, AFUc15224, FGRc16414"				"1.7e-54, 3.0e-53, 8.0e-14, 1.4e-14"			
25827	ENU09622	ANI61C6109: 214..997			GTBX	AFUc09931				2.5E-48			
25828	ENU09623	ANI61C6112: 975..84			GTBX	FGRc04110				5.3E-71			
25829	ENU09624	ANI61C6113: 8..928			GTBX	CALc05352				1.3E-80			
25830	ENU09625	ANI61C6129: 423..1525			GTBX	AFUc07714				4.2E-24			
25831	ENU09626	ANI61S4500: 363..67			GTBX	FGRc05103				5.8E-49			
25832	ENU09627	ANI61C6132: 403..107			GTBX	AFUc01942				1.4E-51			
25833	ENU09628	ANI61S4517: 45..440			GTBX	Y13135				1.5e-38			
25834	ENU09629	ANI61C6140: 51..1322			GTBX	"AFUc00820, Z71256"				"9.1e-23, 8.7e-11"			
25835	ENU09630	ANI61C6142: 1192..107			GTBX	"AFUc05916, CALc05479"				"2.5e-37, 3.4e-110"			
25836	ENU09631	ANI61C6146: 1590..2326			GTBX	"AFUc04896, AFUc05822, FGRc10423"				"1.9e-28, 1.8e-07, 2.7e-13"			
25837	ENU09632	ANI61C5425: 702..94			GTBX	AFUc07579				3.8E-31			
25838	ENU09633	ANI61C6154: 702..1596			GTBX	"AFUc01051, FGRc10010"				"1.2e-18, 1.3e-21"			
25839	ENU09634	ANI61C5426: 761..12			GTBX	"AFUc04407, FGRc10921"				"9.8e-61, 2.0e-47"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25840	ENU09635	ANI61C6157: 2088..1205			GTBX	AFUc14533				6.7E-30			
25841	ENU09636	ANI61C4701: 814..374			GTBX	"AFUc05559, FGRc08592"				"3.7e-89, 2.2e-25"			
25842	ENU09637	ANI61C5430: 1315..803			GTBX	AFUc10737				1.5E-23			
25843	ENU09638	ANI61C4705: 15..1511			GTBX	AFUc13476				2.4E-72			
25844	ENU09639	ANI61C5435: 95..861			GTBX	AFUc14400				1.5E-50			
25845	ENU09640	ANI61C5440: 1234..15			GTBX	U00093				1.4e-111			
25846	ENU09641	ANI61C4712: 606..1352			GTBX	AFUc01145				6.8E-39			
25847	ENU09642	ANI61C6171: 1210..226			GTBX	AFUc15787				5.9E-33			
25848	ENU09643	ANI61C5442: 1738..1020			GTBX	AFUc02895				1.5E-36			
25849	ENU09644	ANI61C5444: 320..668			GTBX	AFUc15322				1E-37			
25850	ENU09645	ANI61C4716: 3235..3650			GTBX	AFUc13372				5.7E-52			
25851	ENU09646	ANI61C5449: 3..537			GTBX	AFUc15317				1.1E-27			
25852	ENU09647	ANI61S3822: 109..415			GTBX	AFUc05500				4.6E-31			
25853	ENU09648	ANI61C4720: 32..475			GTBX	AFUc04498				5E-36			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25854	ENU09649	ANI61C4721: 1773..2670			GTBX	"AFUc08234, AFUc14268"				"1.9e-74, 1.0e-48"			
25855	ENU09650	ANI61C5451: 502..849			GTBX	AFUc21338				2.5E-22			
25856	ENU09651	ANI61C6182: 644..27			GTBX	FGRc06110				2.7E-37			
25857	ENU09652	ANI61C5454: 2..340			GTBX	AFUc06221				5.1E-45			
25858	ENU09653	ANI61C4727: 336..664			GTBX	AFUc12008				4.4E-39			
25859	ENU09654	ANI61C5456: 1126..55			GTBX	"AFUc16901, FGRc10006"				"4.9e-21, 4.5e-14"			
25860	ENU09655	ANI61C6187: 1320..540			GTBX	"AFUc09040, AFUc14490"				"2.5e-144, 3.4e-13"			
25861	ENU09656	ANI61C5458: 571..1412			GTBX	"AFUc07396, AFUc11792, AFUc14619"				"1.9e-11, 1.6e-55, 1.6e-48"			
25862	ENU09657	ANI61C4730: 1349..868			GTBX	"AFUc14839, CALc04948"				"1.1e-22, 1.2e-46"			
25863	ENU09658	ANI61C6190: 1..462			GTBX	AFUc13184				4.5E-69			
25864	ENU09659	ANI61C5464: 911..132			GTBX	"AFUc06054, AFUc20036"				"3.2e-21, 5.2e-22"			
25865	ENU09660	ANI61C4738: 666..33			GTBX	AFUc14106				2.7E-62			
25866	ENU09661	ANI61C4739: 859..2			GTBX	AFUc11624				5.2E-105			
25867	ENU09662	ANI61C6199: 909..1228			GTBX	AFUc13777				4.2E-61			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25868	ENU09663	ANI61C4741: 506..156			GTBX	AFUc22120				1.9E-25			
25869	ENU09664	ANI61C4742: 738..94			GTBX	AFUc10405				1.3E-96			
25870	ENU09665	ANI61C5472: 1135..1935			GTBX	AFUc05296				9E-52			
25871	ENU09666	ANI61C5475: 13..408			GTBX	"AFUc01962, AFUc11850"				"1.8e-20, 2.2e-21"			
25872	ENU09667	ANI61C5475: 1314..662			GTBX	AFUc01962				2.5E-26			
25873	ENU09668	ANI61C4748: 1215..2511			GTBX	AFUc14868				1.2E-119			
25874	ENU09669	ANI61C5479: 620..144			GTBX	AFUc11381				8.9E-37			
25875	ENU09670	ANI61C5479: 1189..2303			GTBX	"AFUc08610, AFUc16734"				"1.5e-107, 1.5e-17"			
25876	ENU09671	ANI61C4756: 407..33			GTBX	AFUc02287				2.2E-21			
25877	ENU09672	ANI61S3867: 266..498			GTBX	AFUc14997				1.3E-26			
25878	ENU09673	ANI61C4761: 56..845			GTBX	AFUc02466				1.2E-26			
25879	ENU09674	ANI61S3872: 446..65			GTBX	AFUc02766				3.3E-42			
25880	ENU09675	ANI61C4771: 1109..62			GTBX	AFUc11383				2.2E-125			
25881	ENU09676	ANI61C4786: 876..135			GTBX	"AFUc15660, FGRc09694"				"4.3e-41, 5.1e-29"			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25882	ENU09677	ANI61C4789: 204..437			GTBX	Y13134				2.5e-14			
25883	ENU09678	ANI61C4789: 1071..690			GTBX	AFUc13817				1.1E-44			
25884	ENU09679	ANI61C4797: 319..2529			GTBX	"AFUc09124, AFUc09640, AFUc18058"				"2.2e-78, 8.8e-38, 8.5e-29"			
25885	ENU09680	ANI61C1103: 26..999			GTBX	FGRc09135				2.7E-37			
25886	ENU09681	ANI61C1105: 13..573			GTBX	"AFUc15843, U00094"				"6.4e-87, 2.8e-40"			
25887	ENU09682	ANI61C1111: 5900..6720			GTBX	"AFUc00779, FGRc22503"				"3.0e-09, 4.3e-35"			
25888	ENU09683	ANI61C1120: 10231..12501			GTBX	"AFUc03712, AFUc18769, CALc03518, FGRc12834, FGRc20309"				"1.2e-22, 8.1e-09, 2.3e-56, 3.5e-13, 6.6e-17"			
25889	ENU09684	ANI61C1121: 4847..3694			GTBX	Y13134				1.3e-41			
25890	ENU09685	ANI61C1123: 2959..23			GTBX	"AFUc00718, AFUc10854, AFUc11508, Z71256"				"2.0e-58, 5.5e-76, 2.5e-19, 1.8e-109"			
25891	ENU09686	ANI61C1126: 2054..1083			GTBX	"AFUc10316, AFUc22327"				"9.7e-40, 5.8e-17"			
25892	ENU09687	ANI61C1132: 3362..6968			GTBX	"AFUc08048, AFUc09981, FGRc03735, Y13136"				"2.3e-128, 4.6e-111, 5.8e-73, 4.3e-166"			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25893	ENU09688	ANI61C1132: 7960..8202			GTBX	AFUc12080				3.2E-39			
25894	ENU09689	ANI61C1133: 3701..5484			GTBX	"AFUc16469, Y13137"				"9.6e-37, 1.2e-44"			
25895	ENU09690	ANI61C1133: 6897..5740			GTBX	FGRc03896				5.8E-55			
25896	ENU09691	ANI61C1138: 12140..10469			GTBX	"AFUc13136, CALc04542"				"8.4e-121, 3.5e-38"			
25897	ENU09692	ANI61C1141: 1383..1990			GTBX	"AFUc22467, FGRc06420"				"1.9e-71, 5.1e-08"			
25898	ENU09693	ANI61C1142: 1359..266			GTBX	AFUc15387				2.7E-96			
25899	ENU09694	ANI61C1145: 338..979			GTBX	"AFUc21496, Y131340"				"2.0e-58, 1.8e-12"			
25900	ENU09695	ANI61C1147: 3448..4162			GTBX	"AFUc06122, CALc05976, FGRc03662"				"1.7e-27, 4.0e-52, 7.5e-53"			
25901	ENU09696	ANI61C1156: 7493..7059			GTBX	AFUc13989				5.7E-25			
25902	ENU09697	ANI61C1161: 553..281			GTBX	FGRc16793				1.1E-44			
25903	ENU09698	ANI61C9802: 3878..2312			GTBX	"FGRc12359, FGRc26682, Y13140"				"5.3e-08, 5.2e-13, 4.4e-67"			
25904	ENU09699	ANI61C9804: 1241..151			GTBX	AFUc03380				2E-46			
25905	ENU09700	ANI61C1178: 878..53			GTBX	AFUc03777				3.4E-26			
25906	ENU09701	ANI61C9810: 1756..1256			GTBX	FGRc23086				1.1E-24			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25907	ENU09702	ANI61C1180: 1196..2056			GTBX	FGRc06851				1.5E-60			
25908	ENU09703	ANI61C1183: 2237..21			GTBX	"AFUc10035, FGRc20878, Y13136"				"2.1e-170, 2.6e-21, 1.1e-68"			
25909	ENU09704	ANI61C1186: 5213..806			GTBX	"AFUc15897, CALc05493"				"0.0, 2.6e-30"			
25910	ENU09705	ANI61C1187: 4140..5351			GTBX	AFUc08928				8.4E-43			
25911	ENU09706	ANI61C1189: 7785..6298			GTBX	"AFUc04073, AFUc20231, AFUc21886"				"1.2e-45, 5.9e-08, 2.4e-27"			
25912	ENU09707	ANI61C9824: 5113..4670			GTBX	AFUc13521				8.2E-33			
25913	ENU09708	ANI61C9826: 1..1518			GTBX	AFUc15367				1.7E-184			
25914	ENU09709	ANI61C9830: 1703..409			GTBX	CALc05806				2.4E-131			
25915	ENU09710	ANI61C9830: 5218..4379			GTBX	AFUc09714				8.1E-24			
25916	ENU09711	ANI61C9834: 6571..7561			GTBX	"AFUc11109, AFUc17602, FGRc08107"				"3.5e-28, 2.1e-19, 6.1e-18"			
25917	ENU09712	ANI61C9836: 947..226			GTBX	"AFUc14827, CALc04616"				"2.2e-16, 3.8e-23"			
25918	ENU09713	ANI61C9839: 611..879			GTBX	AFUc08740				8.4E-22			
25919	ENU09714	ANI61C9847: 1986..2857			GTBX	"AFUc11344, AFUc11344"				"2.9e-45, 4.7e-53"			
25920	ENU09715	ANI61C9847: 4264..3095			GTBX	"AFUc12331, AFUc21805"				"4.6e-31, 6.7e-19"			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25921	ENU09716	ANI61C9847: 9285..10497			GTBX	FGRc11572				9.4E-41			
25922	ENU09717	ANI61C9854: 365..63			GTBX	AFUc20068				2.7E-30			
25923	ENU09718	ANI61C9864: 1801..2743			GTBX	AFUc15416				9.7E-198			
25924	ENU09719	ANI61C9871: 463..701			GTBX	AFUc15546				1.5E-69			
25925	ENU09720	ANI61C9873: 496..2			GTBX	AFUc14820				2.7E-81			
25926	ENU09721	ANI61C9876: 2029..906			GTBX	AFUc13760				2.8E-81			
25927	ENU09722	ANI61C9880: 3365..1981			GTBX	"AFUc06015, FGRc12116"				"6.3e-24, 8.9e-29"			
25928	ENU09723	ANI61C9892: 1057..687			GTBX	"AFUc11408, FGRc01592"				"1.4e-98, 8.4e-10"			
25929	ENU09724	ANI61C6203: 10275..11138			GTBX	AFUc13995				4.9E-165			
25930	ENU09725	ANI61C6205: 2078..1213			GTBX	"AFUc15242, D50617"				"6.6e-108, 1.2e-84"			
25931	ENU09726	ANI61C6213: 2259..580			GTBX	"AFUc02451, AFUc09901, CALc05142, Y13135"				"1.5e-95, 2.4e-19, 6.3e-09, 1.5e-07"			
25932	ENU09727	ANI61C6227: 4483..3758			GTBX	"AFUc03527, AFUc20765"				"2.4e-18, 3.1e-27"			
25933	ENU09728	ANI61C5506: 2022..3044			GTBX	AFUc15489				3.2E-126			
25934	ENU09729	ANI61C5507: 3470..3854			GTBX	AFUc11680				1.2E-40			

GeneWise Gene Annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25935	ENU09730	ANI61C6240: 4..483			GTBX	AFUc01334				5.8E-38			
25936	ENU09731	ANI61C6242: 666..250			GTBX	AFUc06832				1.6E-47			
25937	ENU09732	ANI61S4625: 238..496			GTBX	AFUc15836				9.8E-28			
25938	ENU09733	ANI61C6254: 2036..2560			GTBX	"AFUc10347, AFUc15031"				"1.5e-22, 8.3e-54"			
25939	ENU09734	ANI61C5528: 608..123			GTBX	AFUc13043				7.6E-58			
25940	ENU09735	ANI61C4801: 1188..1772			GTBX	"AFUc01206, AFUc07147, FGRC12821"				"5.6e-24, 2.1e-35, 2.8e-09"			
25941	ENU09736	ANI61C5537: 605..147			GTBX	AFUc15430				3.2E-31			
25942	ENU09737	ANI61C5537: 2786..2061			GTBX	AFUc15185				2.5E-68			
25943	ENU09738	ANI61C5542: 168..530			GTBX	AFUc06476				1.8E-33			
25944	ENU09739	ANI61C4816: 33..461			GTBX	AFUc05360				3.4E-35			
25945	ENU09740	ANI61C5549: 615..1013			GTBX	AFUc05565				7.1E-81			
25946	ENU09741	ANI61C5552: 851..93			GTBX	AFUc14753				2.7E-74			
25947	ENU09742	ANI61C6284: 673..325			GTBX	AFUc09678				2.5E-26			
25948	ENU09743	ANI61S3933: 9..233			GTBX	AFUc11585				7.4E-25			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25949	ENU09744	ANI61C4831: 45..475			GTBX	AFUc13810				3.2E-49			
25950	ENU09745	ANI61C4836: 1112..15			GTBX	AFUc03302				8.9E-93			
25951	ENU09746	ANI61C4837: 4..586			GTBX	AFUc08292				1.2E-92			
25952	ENU09747	ANI61C6297: 2743..3635			GTBX	"AFUc06848, Y13139"				"1.9e-76, 1.2e-25"			
25953	ENU09748	ANI61C6299: 1417..1637			GTBX	AFUc13847				2.2E-59			
25954	ENU09749	ANI61C4840: 108..974			GTBX	AFUc13509				1.9E-118			
25955	ENU09750	ANI61C4849: 942..589			GTBX	FGRc13511				4.8E-29			
25956	ENU09751	ANI61C5582: 44..732			GTBX	CALc06150				6.4E-21			
25957	ENU09752	ANI61C5583: 569..3			GTBX	AFUc20430				1.7E-25			
25958	ENU09753	ANI61C5586: 1296..2030			GTBX	"AFUc06713, FGRc18425"				"4.0e-57, 1.3e-09"			
25959	ENU09754	ANI61C4862: 2887..2038			GTBX	AFUc07470				1.2E-33			
25960	ENU09755	ANI61C4866: 1044..484			GTBX	"AFUc08653, AFUc18008"				"7.0e-62, 1.6e-41"			
25961	ENU09756	ANI61C5596: 623..42			GTBX	AFUc15561				6.3E-42			
25962	ENU09757	ANI61C5598: 478..113			GTBX	Y13137				1.3e-25			

Gene60" description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25963	ENU09758	ANI61C4874: 1487..111			GTBX	AFUc15142				1.4E-124			
25964	ENU09759	ANI61C4879: 1881..1163			GTBX	AFUc08813				1.9E-66			
25965	ENU09760	ANI61C4881: 1028..1734			GTBX	FGRc13484				4E-30			
25966	ENU09761	ANI61C4882: 214..776			GTBX	AFUc06352				2.3E-48			
25967	ENU09762	ANI61C4884: 511..101			GTBX	FGRc04402				1.5E-33			
25968	ENU09763	ANI61C4887: 1783..1230			GTBX	AFUc15282				6.9E-57			
25969	ENU09764	ANI61C4897: 374..1395			GTBX	"AFUc07714, AFUc07747, AFUc11389"				"2.0e-10, 2.8e-32, 5.6e-36"			
25970	ENU09765	ANI61C4899: 258..1409			GTBX	"AFUc12154, FGRc02884"				"3.8e-21, 3.2e-11"			
25971	ENU09766	ANI61S1039: 442..14			GTBX	Y13140				3.5e-39			
25972	ENU09767	ANI61C1205: 437..87			GTBX	AFUc15751				1.5E-53			
25973	ENU09768	ANI61C1208: 6391..8168			GTBX	"AFUc08640, AFUc14702"				"2.8e-95, 4.5e-16"			
25974	ENU09769	ANI61C1208: 8761..10056			GTBX	"AFUc13639, CALc06164"				"5.6e-119, 2.5e-26"			
25975	ENU09770	ANI61C1000 6:478..14			GTBX	AFUc08460				9.9E-21			
25976	ENU09771	ANI61C1000 7:188..676			GTBX	AFUc00879				2.6E-34			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25977	ENU09772	ANI61C1217: 5382..4258			GTBX	AFUc09190				1.7E-68			
25978	ENU09773	ANI61C1001 1:255..7			GTBX	AFUc14823				7.3E-47			
25979	ENU09774	ANI61C1001 5:731..2197			GTBX	AFUc09627				4.7E-29			
25980	ENU09775	ANI61C1223: 2975..2406			GTBX	AFUc10564				1.9E-37			
25981	ENU09776	ANI61C1226: 511..4			GTBX	AFUc15919				1.7E-35			
25982	ENU09777	ANI61C1227: 1799..965			GTBX	"AFUc15619, FGRc18463"				"3.6e-52, 2.4e-39"			
25983	ENU09778	ANI61C1229: 12629..13750			GTBX	"AFUc08495, AFUc15892"				"1.5e-57, 1.2e-44"			
25984	ENU09779	ANI61C1002 0:14..511			GTBX	"AFUc18869, CALc02488"				"1.1e-74, 5.1e-52"			
25985	ENU09780	ANI61C1002 5:1419..2136			GTBX	"AFUc11304, AFUc11498, AFUc15909"				"7.6e-27, 3.8e-36, 2.4e-40"			
25986	ENU09781	ANI61C1002 6:2060..4211			GTBX	"AFUc09022, AFUc11200, FGRc09828"				"1.1e- 155, 3.6e-09, 7.7e-30"			
25987	ENU09782	ANI61C1002 8:8..556			GTBX	FGRc10845				7.3E-23			
25988	ENU09783	ANI61C1234: 698..264			GTBX	FGRc03585				2.7E-22			
25989	ENU09784	ANI61C1236: 3294..247			GTBX	"CALc05504, CALc05504, FGRc10685"				"1.1e- 166, 4.4e- 172, 1.0e-24"			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25990	ENU09785	ANI61C1003 9:78..593			GTBX	AFUc04205				2.2E-29			
25991	ENU09786	ANI61C1243: 76..647			GTBX	AFUc14226				2.2E-47			
25992	ENU09787	ANI61C1244: 639..205			GTBX	AFUc10187				4.6E-49			
25993	ENU09788	ANI61C1004 3:638..1321			GTBX	AFUc11890				3.5E-128			
25994	ENU09789	ANI61C1004 3:4533..1878			GTBX	"AFUc18915, AFUc22245, CALc06125"				"2.9e-37, 5.4e-55, 6.3e-86"			
25995	ENU09790	ANI61S1082: 533..81			GTBX	"AFUc14265, AFUc15053, CALc06148"				"3.6e-09, 1.1e-45, 1.8e-46"			
25996	ENU09791	ANI61C1004 8:1235..1896			GTBX	"AFUc17530, AFUc21626"				"9.1e-23, 4.6e-18"			
25997	ENU09792	ANI61S1086: 306..22			GTBX	AFUc10933				2.8E-39			
25998	ENU09793	ANI61C1250: 965..442			GTBX	AFUc02186				2.9E-64			
25999	ENU09794	ANI61C1251: 435..235			GTBX	AFUc05890				1.8E-31			
26000	ENU09795	ANI61C1460: 658..362			TBX	AFUc04191				1.4E-57			
26001	ENU09796	ANI61C1026 8:2016..2441			TBX	AFUc05348				1.5E-36			
26002	ENU09797	ANI61C1472: 2305..2820			TBX	AFUc15503				3.8E-62			
26003	ENU09798	ANI61C1473: 744..469			TBX	AFUc05026				1.1E-51			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26004	ENU09799	ANI61C1473:1063..845			TBX	AFUc05026				1.1E-51			
26005	ENU09800	ANI61C1027 6:1572..2084			TBX	AFUc13815				6.7E-37			
26006	ENU09801	ANI61C1484:2614..3107			TBX	AFUc22069				3.7E-37			
26007	ENU09802	ANI61C1028 2:741..950			TBX	AFUc14473				1.3E-129			
26008	ENU09803	ANI61C1028 3:939..666			TBX	AFUc10944				7.2E-84			
26009	ENU09804	ANI61C1028 9:873..166			TBX	AFUc14293				3.4E-59			
26010	ENU09805	ANI61C322:2 318..2686			TBX	Y13138				1.7e-18			
26011	ENU09806	ANI61C349:9 981..9772			TBX	AFUc08818				8.1E-69			
26012	ENU09807	ANI61C352:5 292..5651			TBX	AFUc05906				1.5E-41			
26013	ENU09808	ANI61C363:3 04..2			TBX	CALc02816				1.9E-35			
26014	ENU09809	ANI61C7202:134..361			TBX	AFUc14285				1E-31			
26015	ENU09810	ANI61C7216:1390..1924			TBX	"AFUc11696, AFUc11696"				"1.7e-61, 4.9e-33"			
26016	ENU09811	ANI61C7219:2645..2310			TBX	AFUc09975				1.4E-59			
26017	ENU09812	ANI61C385:4 260..4942			TBX	AFUc12528				2.5E-53			

Gene Description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26018	ENU09813	ANI61C388:4 66..64			TBX	AFUc20119				1.2E-55			
26019	ENU09814	ANI61C7223: 2972..2172			TBX	AFUc06424				1.1E-58			
26020	ENU09815	ANI61C7224: 4437..4850			TBX	AFUc12875				3.1E-88			
26021	ENU09816	ANI61C7236: 1466..1086			TBX	AFUc18591				3.4E-42			
26022	ENU09817	ANI61C7238: 680..344			TBX	AFUc09528				2.5E-45			
26023	ENU09818	ANI61C7238: 1092..832			TBX	AFUc09528				2.5E-45			
26024	ENU09819	ANI61C7271: 1132..605			TBX	AFUc06636				2.4E-38			
26025	ENU09820	ANI61C7272: 1371..1610			TBX	AFUc07449				1.1E-44			
26026	ENU09821	ANI61C5818: 881..339			TBX	AFUc08233				7.7E-38			
26027	ENU09822	ANI61S204:4 81..27			TBX	FGRc12216				3.7E-40			
26028	ENU09823	ANI61C7285: 8248..8667			TBX	AFUc15172				4.4E-69			
26029	ENU09824	ANI61C5830: 16..802			TBX	AFUc08094				2.6E-48			
26030	ENU09825	ANI61C6560: 32..1156			TBX	AFUc13931				1.4E-79			
26031	ENU09826	ANI61C5832: 1096..497			TBX	AFUc08734				4.3E-50			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26032	ENU09827	ANI61C5833: 388..56			TBX	AFUc14136				5.3E-62			
26033	ENU09828	ANI61C5839: 1627..1427			TBX	FGRc09504				1.8E-33			
26034	ENU09829	ANI61C5884: 2..364			TBX	AFUc15412				1.3E-35			
26035	ENU09830	ANI61C5887: 983..1786			TBX	AFUc04019				2.4E-62			
26036	ENU09831	ANI61S1313: 480..60			TBX	AFUc15343				2E-56			
26037	ENU09832	ANI61C2211: 862..1176			TBX	AFUc14418				1.1E-61			
26038	ENU09833	ANI61C2212: 4052..2947			TBX	"AFUc11116, AFUc12982"				"2.5e-97, 1.1e-57"			
26039	ENU09834	ANI61C2212: 4426..4133			TBX	AFUc11116				2.5E-97			
26040	ENU09835	ANI61C1103 1:2217..2515			TBX	AFUc13932				2.9E-51			
26041	ENU09836	ANI61C1030 2:13980..1419 5			TBX	AFUc15817				9.2E-172			
26042	ENU09837	ANI61C1030 2:3197..2559			TBX	AFUc13294				4.2E-40			
26043	ENU09838	ANI61C1030 2:14598..1423 3			TBX	AFUc15817				4.4E-207			
26044	ENU09839	ANI61C1103 2:5852..6235			TBX	"AFUc15294, AFUc22376, AFUc22376"				"1.1e-91, 2.0e-08, 3.0e-18"			
26045	ENU09840	ANI61C1103 7:2465..2914			TBX	AFUc01826				7.6E-34			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26046	ENU09841	ANI61C2243: 321..63			TBX	AFUc04253				4.2E-93			
26047	ENU09842	ANI61C1031 8:6871..7170			TBX	AFUc08903				3E-41			
26048	ENU09843	ANI61C2250: 27..410			TBX	AFUc14478				8.6E-55			
26049	ENU09844	ANI61C1032 1:4802..5332			TBX	AFUc13535				1.4E-70			
26050	ENU09845	ANI61C1105 1:1650..1889			TBX	AFUc15849				3.5E-49			
26051	ENU09846	ANI61C1105 6:1..393			TBX	AFUc10621				4E-68			
26052	ENU09847	ANI61S1369: 2..411			TBX	AFUc15183				1.2E-41			
26053	ENU09848	ANI61C1033 0:13..225			TBX	FGRc08647				3.6E-42			
26054	ENU09849	ANI61C1033 5:2001..2270			TBX	AFUc11528				6E-153			
26055	ENU09850	ANI61C1106 5:1976..3091			TBX	AFUc12698				1.3E-138			
26056	ENU09851	ANI61C1033 8:652..1062			TBX	AFUc15802				5.7E-81			
26057	ENU09852	ANI61C1034 3:382..104			TBX	AFUc15194				1.2E-194			
26058	ENU09853	ANI61C1555: 1459..1665			TBX	AFUc09094				2.2E-48			
26059	ENU09854	ANI61S1393: 3..350			TBX	AFUc11981				8.7E-34			

Sequence Alignment

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26060	ENU09855	ANI61C1035 7:2937..1118			TBX	"AFUc10516, AFUc13253"				"1.4e-96, 1.1e-16"			
26061	ENU09856	ANI61C1035 8:2452..2676			TBX	AFUc21007				4.8E-39			
26062	ENU09857	ANI61S1397: 31..342			TBX	AFUc15972				6.6E-38			
26063	ENU09858	ANI61C1564: 1067..1316			TBX	AFUc03100				1.6E-71			
26064	ENU09859	ANI61C1036 0:1291..1680			TBX	AFUc05803				7.4E-36			
26065	ENU09860	ANI61C1036 0:3349..3570			TBX	AFUc13299				2.7E-142			
26066	ENU09861	ANI61C1036 0:385..1			TBX	AFUc15643				5.5E-39			
26067	ENU09862	ANI61C1036 0:3316..3017			TBX	AFUc13299				1.5E-150			
26068	ENU09863	ANI61C1109 9:1051..1761			TBX	AFUc13178				1.2E-56			
26069	ENU09864	ANI61C1109 9:10567..1015 4			TBX	"AFUc04105, FGRc12288"				"3.7e-16, 1.1e-57"			
26070	ENU09865	ANI61C403:1 218..1006			TBX	AFUc02462				1.9E-60			
26071	ENU09866	ANI61C1037 0:104..925			TBX	AFUc11594				1.7E-49			
26072	ENU09867	ANI61C1585: 92..490			TBX	AFUc15700				3.3E-38			
26073	ENU09868	ANI61C410:7 738..8487			TBX	"AFUc04942, AFUc11941, CALc04450"				"1.1e-67, 1.3e-34, 3.5e-29"			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26074	ENU09869	ANI61C412:1 440..1774			TBX	AFUc05418				3.7E-70			
26075	ENU09870	ANI61C412:6 523..6927			TBX	AFUc11022				4.3E-57			
26076	ENU09871	ANI61C412:7 008..7352			TBX	AFUc11022				4.3E-57			
26077	ENU09872	ANI61C1038 6:1631..1945			TBX	AFUc10295				1E-42			
26078	ENU09873	ANI61C1038 6:1945..2298			TBX	AFUc10295				1E-42			
26079	ENU09874	ANI61C1038 7:55..495			TBX	AFUc15010				5.6E-58			
26080	ENU09875	ANI61C1593: 241..771			TBX	AFUc02879				6.4E-48			
26081	ENU09876	ANI61C425:5 20..95			TBX	AFUc15422				1.5E-38			
26082	ENU09877	ANI61C431:3 2..613			TBX	AFUc03600				1.3E-33			
26083	ENU09878	ANI61C433:3 511..3186			TBX	CALc05879				9E-80			
26084	ENU09879	ANI61C8004: 2247..1915			TBX	AFUc12803				1.8E-113			
26085	ENU09880	ANI61C445:2 3..278			TBX	Y13139				5.9e-57			
26086	ENU09881	ANI61C8028: 409..2			TBX	Y13137				5.9e-75			
26087	ENU09882	ANI61C8033: 60..272			TBX	Z71256				2.7e-59			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26088	ENU09883	ANI61C7309: 548..3			TBX	AFUc12240				2.7E-59			
26089	ENU09884	ANI61C7317: 2202..1795			TBX	FGRc01319				1.5E-44			
26090	ENU09885	ANI61C7317: 2579..2337			TBX	AFUc11246				7E-49			
26091	ENU09886	ANI61C7318: 1943..1584			TBX	AFUc11373				1.3E-32			
26092	ENU09887	ANI61C481:8 0..589			TBX	AFUc14011				5.6E-45			
26093	ENU09888	ANI61C8051: 469..212			TBX	CALc04459				3E-62			
26094	ENU09889	ANI61C8051: 6074..5853			TBX	Z71256				1.2e-82			
26095	ENU09890	ANI61C8053: 2264..2734			TBX	AFUc14405				2E-57			
26096	ENU09891	ANI61C499:7 22..455			TBX	AFUc09357				1.1E-68			
26097	ENU09892	ANI61C7331: 4599..4327			TBX	AFUc15784				3E-39			
26098	ENU09893	ANI61C6614: 1629..1394			TBX	AFUc15221				1.2E-142			
26099	ENU09894	ANI61C6621: 1600..1818			TBX	CALc06130				4.9E-55			
26100	ENU09895	ANI61C8084: 3162..3470			TBX	AFUc15749				8.8E-31			
26101	ENU09896	ANI61C8085: 96..612			TBX	AFUc17865				1.2E-53			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26102	ENU09897	ANI61C7356: 26..235			TBX	AFUc14910				7.6E-172			
26103	ENU09898	ANI61C8087: 771..1			TBX	AFUc12758				4.4E-32			
26104	ENU09899	ANI61C6632: 431..192			TBX	AFUc06255				5.4E-64			
26105	ENU09900	ANI61C7365: 8009..7809			TBX	AFUc05380				1.5E-42			
26106	ENU09901	ANI61C5911: 1563..1063			TBX	AFUc14011				1.3E-36			
26107	ENU09902	ANI61C6644: 572..294			TBX	AFUc15344				4.4E-98			
26108	ENU09903	ANI61C7394: 1580..1083			TBX	AFUc10645				2.5E-63			
26109	ENU09904	ANI61C7396: 6555..7882			TBX	"AFUc08731, FGRc07479"				"3.5e-64, 1.9e-59"			
26110	ENU09905	ANI61C6667: 233..10			TBX	AFUc08889				4.1E-44			
26111	ENU09906	ANI61C5941: 871..323			TBX	AFUc05668				8.3E-43			
26112	ENU09907	ANI61C6677: 395..21			TBX	AFUc12033				2.1E-47			
26113	ENU09908	ANI61C5957: 429..757			TBX	AFUc00567				2.7E-65			
26114	ENU09909	ANI61C5967: 9075..9284			TBX	FGRc11859				1.8E-32			
26115	ENU09910	ANI61S2104: 550..7			TBX	"AFUc04034, FGRc16556"				"2.6e-39, 1.1e-16"			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	% Description
26116	ENU09911	ANI61C5978: 275..3			TBX	AFUc03602				1.2E-61			
26117	ENU09912	ANI61C3001: 411..2			TBX	AFUc15002				2.1E-49			
26118	ENU09913	ANI61C5997: 990..478			TBX	AFUc10036				1.3E-33			
26119	ENU09914	ANI61C3026: 568..11			TBX	"AFUc15479, AFUc21770"				"7.6e-22, 1.9e-35"			
26120	ENU09915	ANI61C2305: 1105..612			TBX	AFUc11158				3.1E-32			
26121	ENU09916	ANI61C1110 7:652..155			TBX	AFUc22275				1E-32			
26122	ENU09917	ANI61C1110 7:8686..8456			TBX	AFUc14504				2.9E-41			
26123	ENU09918	ANI61C3046: 869..252			TBX	AFUc09171				7.2E-40			
26124	ENU09919	ANI61C2324: 416..628			TBX	AFUc11776				3.4E-81			
26125	ENU09920	ANI61C3056: 3382..2980			TBX	"AFUc10340, CALc05472"				"1.3e-14, 4.3e-61"			
26126	ENU09921	ANI61C3062: 983..432			TBX	AFUc07103				2.5E-94			
26127	ENU09922	ANI61C2334: 764..1012			TBX	AFUc02776				5.2E-57			
26128	ENU09923	ANI61C1113 3:4764..4195			TBX	AFUc21395				4E-40			
26129	ENU09924	ANI61C1040 5:4666..4179			TBX	AFUc15972				3.2E-48			

Gene annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26144	ENU09939	ANI61C1118 3:581..4			TBX	AFUc07733				9.6E-52			
26145	ENU09940	ANI61C1045 5:1831..2178			TBX	AFUc13075				5.4E-56			
26146	ENU09941	ANI61C1118 5:3141..2914			TBX	AFUc13895				3.2E-107			
26147	ENU09942	ANI61C1118 6:2201..1884			TBX	AFUc13910				2.3E-33			
26148	ENU09943	ANI61C1118 9:880..1347			TBX	AFUc05827				2.1E-56			
26149	ENU09944	ANI61C1668: 961..1218			TBX	AFUc03564				5.9E-31			
26150	ENU09945	ANI61C1668: 1423..2232			TBX	"AFUc03564, AFUc19776"				"5.9e-31, 2.6e-46"			
26151	ENU09946	ANI61C1119 3:724..206			TBX	AFUc03276				6.8E-64			
26152	ENU09947	ANI61C1046 4:16..517			TBX	AFUc14564				1.5E-68			
26153	ENU09948	ANI61C508:2 833..2485			TBX	AFUc12712				2.7E-34			
26154	ENU09949	ANI61C1047 7:7766..8083			TBX	AFUc15740				3.3E-55			
26155	ENU09950	ANI61C1047 7:10845..11214			TBX	"AFUc13557, X59720"				"3.1e-53, 8.7e-50"			
26156	ENU09951	ANI61C1048 3:1906..2700			TBX	AFUc15804				7.7E-153			
26157	ENU09952	ANI61C1048 3:3278..3486			TBX	"AFUc15804, AFUc15804"				"4.0e-150, 7.7e-153"			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	Description
26172	ENU09967	ANI61C8133:3..473			TBX	AFUc11118				4.2E-59			
26173	ENU09968	ANI61C578:577..1029			TBX	AFUc01862				3.6E-64			
26174	ENU09969	ANI61C8140:938..64			TBX	"AFUc00985, AFUc03101"				"1.7e-16, 6.6e-43"			
26175	ENU09970	ANI61C7419:511..140			TBX	AFUc15103				2.7E-52			
26176	ENU09971	ANI61C7419:1006..668			TBX	AFUc15103				2.7E-52			
26177	ENU09972	ANI61C8155:2..232			TBX	AFUc15172				2.4E-43			
26178	ENU09973	ANI61C592:459..1			TBX	FGRc12433				5.6E-42			
26179	ENU09974	ANI61C7430:1250..1047			TBX	AFUc05191				3.2E-97			
26180	ENU09975	ANI61C6703:847..1110			TBX	AFUc14632				7.8E-86			
26181	ENU09976	ANI61C6703:2316..1740			TBX	AFUc14632				3.3E-72			
26182	ENU09977	ANI61C6709:4001..4468			TBX	AFUc03350				2.4E-52			
26183	ENU09978	ANI61C6711:2059..1173			TBX	AFUc14433				2.9E-154			
26184	ENU09979	ANI61C6711:2772..2153			TBX	AFUc14433				2.9E-154			
26185	ENU09980	ANI61C6714:6174..6386			TBX	AFUc14412				4.5E-35			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26186	ENU09981	ANI61C6717: 1667..1895			TBX	Y13138				2.8e-34			
26187	ENU09982	ANI61C7455: 2801..2121			TBX	AFUc14993				5.7E-52			
26188	ENU09983	ANI61C6728: 254..499			TBX	AFUc04684				2E-44			
26189	ENU09984	ANI61C7465: 74..283			TBX	AFUc14734				2.8E-136			
26190	ENU09985	ANI61C7485: 3034..3324			TBX	AFUc13156				5.2E-35			
26191	ENU09986	ANI61C7492: 14..599			TBX	AFUc08563				1E-93			
26192	ENU09987	ANI61C6764: 431..997			TBX	AFUc02841				1.4E-59			
26193	ENU09988	ANI61C6772: 1885..1670			TBX	AFUc13631				5E-78			
26194	ENU09989	ANI61C6772: 3366..2850			TBX	AFUc11189				2.3E-31			
26195	ENU09990	ANI61C6777: 1739..2320			TBX	AFUc11182				9.5E-73			
26196	ENU09991	ANI61C6779: 885..415			TBX	AFUc01472				8.6E-45			
26197	ENU09992	ANI61C6785: 400..657			TBX	AFUc18290				1.8E-60			
26198	ENU09993	ANI61S2209: 584..63			TBX	AFUc12936				4.4E-55			
26199	ENU09994	ANI61C3104: 3733..3464			TBX	Y13134				1.1e-95			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26200	ENU09995	ANI61C3122: 355..765			TBX	AFUc15397				3.3E-72			
26201	ENU09996	ANI61C2410: 1111..1348			TBX	AFUc10475				9E-39			
26202	ENU09997	ANI61C2410: 1841..2470			TBX	"AFUc14120, AFUc14120"				"1.3e-116, 1.8e-98"			
26203	ENU09998	ANI61C1121 7:429..1			TBX	CALc01737				5.9E-34			
26204	ENU09999	ANI61C3151: 766..1116			TBX	AFUc12817				1.4E-34			
26205	ENU10000	ANI61C1122 5:2..694			TBX	AFUc11815				3.1E-62			
26206	ENU10001	ANI61C1122 5:879..1377			TBX	"AFUc11815, AFUc11815"				"2.4e-54, 3.1e-62"			
26207	ENU10002	ANI61C1122 9:3671..2959			TBX	AFUc15733				1.7E-120			
26208	ENU10003	ANI61C1700: 23..397			TBX	AFUc13133				3.5E-35			
26209	ENU10004	ANI61C1701: 2076..2837			TBX	AFUc15352				1.3E-62			
26210	ENU10005	ANI61C1705: 3399..3761			TBX	AFUc08134				1.8E-44			
26211	ENU10006	ANI61C2436: 957..1347			TBX	AFUc15614				2.4E-85			
26212	ENU10007	ANI61C1123 4:467..3			TBX	AFUc15455				2.2E-40			
26213	ENU10008	ANI61C1124 0:2..461			TBX	AFUc06703				9.7E-46			

[illegible]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr	g Description
26214	ENU10009	ANI61C3182:2031..2377			TBX	AFUc04772				7E-47			
26215	ENU10010	ANI61C3185:508..145			TBX	AFUc13049				1.7E-126			
26216	ENU10011	ANI61C3186:3106..2741			TBX	AFUc13434				7.6E-45			
26217	ENU10012	ANI61C1730:3..527			TBX	AFUc10266				6.5E-59			
26218	ENU10013	ANI61C3191:278..3			TBX	AFUc15545				3.8E-87			
26219	ENU10014	ANI61C2464:1668..1021			TBX	FGRc11747				1.2E-31			
26220	ENU10015	ANI61C3199:1..611			TBX	AFUc15519				1.3E-45			
26221	ENU10016	ANI61C1741:618..33			TBX	AFUc15826				8.6E-41			
26222	ENU10017	ANI61C2473:1109..42			TBX	"AFUc09645, AFUc09645"				"3.3e-31, 7.9e-54"			
26223	ENU10018	ANI61C10541:2933..2106			TBX	"AFUc12046, Y13140"				"6.8e-95, 3.0e-130"			
26224	ENU10019	ANI61C11274:1813..796			TBX	"FGRc06649, FGRc11623"				"3.8e-34, 9.9e-11"			
26225	ENU10020	ANI61C11279:17..250			TBX	AFUc07741				8.7E-61			
26226	ENU10021	ANI61C2480:240..440			TBX	AFUc08744				6.3E-48			
26227	ENU10022	ANI61C1759:1431..460			TBX	"AFUc11420, AFUc18306"				"3.8e-51, 2.0e-21"			

[illegible]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26228	ENU10023	ANI61C1055 3:21..320			TBX	CALc06110				8.7E-101			
26229	ENU10024	ANI61C1055 5:2699..1999			TBX	AFUc05645				8.4E-74			
26230	ENU10025	ANI61C1055 7:467..96			TBX	AFUc13557				6.9E-52			
26231	ENU10026	ANI61C2495: 521..3			TBX	AFUc14306				2.3E-76			
26232	ENU10027	ANI61C600:2 174..1764			TBX	CALc06158				1.5E-72			
26233	ENU10028	ANI61C602:9 74..355			TBX	AFUc13158				1.2E-65			
26234	ENU10029	ANI61C1057 2:57..1135			TBX	"AFUc00606, AFUc06517, FGRc10385"				"1.3e-12, 1.3e-51, 1.0e-33"			
26235	ENU10030	ANI61C1057 3:1024..1449			TBX	AFUc03864				2.5E-83			
26236	ENU10031	ANI61C613:3 ..584			TBX	AFUc14174				1.1E-67			
26237	ENU10032	ANI61C1058 2:545..72			TBX	AFUc14725				2.9E-38			
26238	ENU10033	ANI61C1058 9:7928..8383			TBX	AFUc13200				3.3E-98			
26239	ENU10034	ANI61C1059 2:2426..2656			TBX	AFUc07883				9.4E-32			
26240	ENU10035	ANI61C634:8 86..629			TBX	Y13136				1.0e-18			
26241	ENU10036	ANI61C656:3 4..618			TBX	AFUc07639				1.2E-64			

GenBank

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26242	ENU10037	ANI61C669:3 23..48			TBX	AFUc11626				1.7E-36			
26243	ENU10038	ANI61C8230: 165..455			TBX	FGRcl1456				1.9E-37			
26244	ENU10039	ANI61C7508: 1555..372			TBX	AFUc09787				6.4E-78			
26245	ENU10040	ANI61C671:4 82..808			TBX	AFUc15558				4.8E-61			
26246	ENU10041	ANI61C686:4 695..5262			TBX	AFUc13870				7.5E-43			
26247	ENU10042	ANI61C7523: 1790..2362			TBX	AFUc06950				1.4E-52			
26248	ENU10043	ANI61C7528: 395..3			TBX	AFUc15740				1.2E-39			
26249	ENU10044	ANI61C699:3 53..2			TBX	AFUc09402				3.2E-44			
26250	ENU10045	ANI61C7530: 972..442			TBX	AFUc11771				2.1E-55			
26251	ENU10046	ANI61C7531: 2779..3147			TBX	CALc05550				1.4E-32			
26252	ENU10047	ANI61C7535: 548..1081			TBX	AFUc15071				2.3E-118			
26253	ENU10048	ANI61C7535: 380..3			TBX	AFUc13442				4.5E-43			
26254	ENU10049	ANI61C6808: 2162..2704			TBX	AFUc13976				5.2E-32			

GenBank

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26255	ENU10050	ANI61C6814: 3423..1721			TBX	"AFUc06527, AFUc17241, FGRc09905, FGRc15187"				"1.8e-113, 5.7e-40, 2.6e-74, 3.5e-13"			
26256	ENU10051	ANI61C8273: 1404..1688			TBX	FGRc12425				1.8E-170			
26257	ENU10052	ANI61C8273: 3873..3640			TBX	AFUc11234				7.4E-91			
26258	ENU10053	ANI61C8273: 4919..4605			TBX	AFUc04450				5.2E-32			
26259	ENU10054	ANI61C7546: 569..9			TBX	Y13140				1.5e-69			
26260	ENU10055	ANI61C6819: 360..61			TBX	AFUc14565				1.9E-86			
26261	ENU10056	ANI61C6819: 1172..511			TBX	"AFUc14565, AFUc14565"				"1.9e-86, 5.6e-26"			
26262	ENU10057	ANI61C6823: 475..86			TBX	AFUc08494				3.4E-57			
26263	ENU10058	ANI61C6827: 1241..709			TBX	AFUc15969				9.6E-34			
26264	ENU10059	ANI61C7560: 710..153			TBX	AFUc14056				3.6E-33			
26265	ENU10060	ANI61C8293: 1736..1422			TBX	AFUc11416				4.3E-66			
26266	ENU10061	ANI61C6867: 4199..4710			TBX	AFUc13638				2.6E-33			
26267	ENU10062	ANI61C6875: 487..239			TBX	AFUc15186				2.1E-45			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26268	ENU10063	ANI61C6880:422..6			TBX	AFUc09175				3.8E-41			
26269	ENU10064	ANI61C6892:286..771			TBX	AFUc01364				1.2E-43			
26270	ENU10065	ANI61C6895:48..635			TBX	AFUc20237				3.8E-48			
26271	ENU10066	ANI61C3208:2018..2563			TBX	AFUc10936				5.8E-66			
26272	ENU10067	ANI61S3046:93..596			TBX	AFUc15363				4.9E-51			
26273	ENU10068	ANI61C3229:2533..2303			TBX	AFUc08535				1.3E-33			
26274	ENU10069	ANI61C2509:3278..2802			TBX	AFUc14181				8.3E-66			
26275	ENU10070	ANI61C3241:1482..1832			TBX	AFUc11766				4.3E-36			
26276	ENU10071	ANI61C11311:1269..1808			TBX	AFUc07214				9.1E-36			
26277	ENU10072	ANI61C3253:1238..2259			TBX	AFUc15072				7.1E-105			
26278	ENU10073	ANI61C11321:1517..2423			TBX	AFUc10674				3.3E-98			
26279	ENU10074	ANI61S1636:335..3			TBX	AFUc02091				6.5E-41			
26280	ENU10075	ANI61C2549:36..604			TBX	FGRc12323				5.1E-35			
26281	ENU10076	ANI61C11341:3722..3447			TBX	CALc05684				4.8E-52			

GenBank

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26282	ENU10077	ANI61S1654:1..347			TBX	AFUc10087				5.9E-35			
26283	ENU10078	ANI61C2553:14..374			TBX	AFUc05589				2.6E-44			
26284	ENU10079	ANI61C2553:2527..3117			TBX	AFUc04288				5.7E-58			
26285	ENU10080	ANI61C10624:2670..2122			TBX	AFUc09584				5.6E-35			
26286	ENU10081	ANI61C11357:34..367			TBX	AFUc15619				3.2E-42			
26287	ENU10082	ANI61C1836:516..7			TBX	Z71256				2.7e-20			
26288	ENU10083	ANI61C3299:772..1486			TBX	AFUc15114				9.9E-61			
26289	ENU10084	ANI61C10634:3..416			TBX	FGRC10919				2.1E-33			
26290	ENU10085	ANI61C11363:2..495			TBX	AFUc13573				2.3E-64			
26291	ENU10086	ANI61S1673:438..133			TBX	AFUc01485				2E-37			
26292	ENU10087	ANI61C1840:506..42			TBX	AFUc09670				3.8E-37			
26293	ENU10088	ANI61C10646:757..247			TBX	AFUc10676				1.9E-70			
26294	ENU10089	ANI61C10646:1379..1034			TBX	AFUc10676				1.9E-70			
26295	ENU10090	ANI61C1850:1015..1			TBX	AFUc15969				3.6E-101			

Table 6.10. Continued

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26296	ENU10091	ANI61C1065 4:5628..6366			TBX	"AFUc15290, FGRc03192"				"1.0e-153, 1.6e-66" 2.1E-47			
26297	ENU10092	ANI61C1138 4:961..456			TBX	AFUc04784							
26298	ENU10093	ANI61C1138 6:949..477			TBX	AFUc07894				1.8E-51			
26299	ENU10094	ANI61C2598: 1649..1030			TBX	AFUc14134				3.8E-61			
26300	ENU10095	ANI61C1139 3:1062..1801			TBX	"AFUc15965, AFUc15965"				"1.4e-160, 4.5e-167" 4.5E-167			
26301	ENU10096	ANI61C1139 3:2717..3327			TBX	AFUc15965							
26302	ENU10097	ANI61C1139 3:3454..4047			TBX	AFUc15965				4.5E-167			
26303	ENU10098	ANI61C1139 8:1407..1883			TBX	AFUc19996				5.4E-33			
26304	ENU10099	ANI61C1066 9:2650..2192			TBX	AFUc15856				2E-118			
26305	ENU10100	ANI61C1871: 642..304			TBX	AFUc01385				3.1E-34			
26306	ENU10101	ANI61C702:9 ..296			TBX	AFUc02664				2.3E-50			
26307	ENU10102	ANI61C1067 0:241..2			TBX	AFUc11950				5.1E-41			
26308	ENU10103	ANI61C9007: 3904..4113			TBX	AFUc13744				2.2E-85			
26309	ENU10104	ANI61C1886: 516..781			TBX	AFUc12305				9.9E-50			

Contig contigs

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26310	ENU10105	ANI61C1068 6:674..357			TBX	AFUc16162				1.5E-45			
26311	ENU10106	ANI61C1899: 1..216			TBX	X59720				5.9e-45			
26312	ENU10107	ANI61C722:3 540..3286			TBX	Y13134				2.1e-120			
26313	ENU10108	ANI61C1069 1:232..450			TBX	AFUc01808				1.2E-43			
26314	ENU10109	ANI61C1069 2:1866..2621			TBX	AFUc15403				9.5E-47			
26315	ENU10110	ANI61C9024: 334..2			TBX	AFUc10157				2.4E-73			
26316	ENU10111	ANI61C736:4 ..557			TBX	FGRc08015				4.1E-34			
26317	ENU10112	ANI61C742:9 86..1309			TBX	AFUc04230				2.2E-42			
26318	ENU10113	ANI61C9041: 769..225			TBX	AFUc15972				4.3E-51			
26319	ENU10114	ANI61C8314: 847..1149			TBX	AFUc01794				9.8E-39			
26320	ENU10115	ANI61C754:1 694..2598			TBX	AFUc07695				6E-94			
26321	ENU10116	ANI61C759:9 74..1656			TBX	AFUc15782				1.3E-216			
26322	ENU10117	ANI61C760:8 24..1195			TBX	AFUc15173				7.7E-116			
26323	ENU10118	ANI61C9060: 489..1082			TBX	"AFUc09562, AFUc16430"				"5.1e-41, 1.7e-14"			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26324	ENU10119	ANI61C7602: 2..661			TBX	AFUc08499				2E-43			
26325	ENU10120	ANI61C7611: 266..18			TBX	AFUc01029				1E-34			
26326	ENU10121	ANI61C9078: 1169..627			TBX	"CALc05486, Y13140"				"1.7e-172, 9.9e-187"			
26327	ENU10122	ANI61C9081: 2..544			TBX	AFUc09562				3.3E-71			
26328	ENU10123	ANI61C796:2 000..1580			TBX	Z71256				1.1e-94			
26329	ENU10124	ANI61C797:3 073..3285			TBX	AFUc14002				2E-68			
26330	ENU10125	ANI61C6901: 369..1157			TBX	AFUc11697				1.6E-66			
26331	ENU10126	ANI61C6908: 238..2			TBX	AFUc11236				2E-80			
26332	ENU10127	ANI61C8372: 68..310			TBX	FGRc10332				2.9E-38			
26333	ENU10128	ANI61C6936: 1145..1738			TBX	AFUc00849				5.3E-50			
26334	ENU10129	ANI61C6941: 1300..322			TBX	AFUc13344				4.8E-76			
26335	ENU10130	ANI61C7675: 1507..1737			TBX	AFUc15563				2.7E-84			
26336	ENU10131	ANI61S617:5 00..105			TBX	AFUc05623				7E-47			
26337	ENU10132	ANI61C24:48 2..219			TBX	AFUc10888				2.2E-38			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26338	ENU10133	ANI61C24:39 12..3514			TBX	AFUc03140				3E-62			
26339	ENU10134	ANI61C4002: 2009..1581			TBX	AFUc10817				4.7E-59			
26340	ENU10135	ANI61C6983: 961..1700			TBX	AFUc14695				1E-47			
26341	ENU10136	ANI61C4013: 122..460			TBX	AFUc11715				4.5E-34			
26342	ENU10137	ANI61C6992: 2612..3298			TBX	AFUc10584				8.8E-42			
26343	ENU10138	ANI61C4029: 80..709			TBX	AFUc13720				5.9E-36			
26344	ENU10139	ANI61C4034: 851..537			TBX	FGRc12892				3.8E-40			
26345	ENU10140	ANI61C74:24 01..1973			TBX	FGRc10359				2E-50			
26346	ENU10141	ANI61C80:31 13..3924			TBX	AFUc11668				1.9E-71			
26347	ENU10142	ANI61C82:17 26..1385			TBX	AFUc06769				3.8E-51			
26348	ENU10143	ANI61C4062: 745..1218			TBX	AFUc07689				5.4E-37			
26349	ENU10144	ANI61C95:21 13..1149			TBX	FGRc02814				5.6E-52			
26350	ENU10145	ANI61C96:15 17..1230			TBX	FGRc10078				1.4E-40			
26351	ENU10146	ANI61C1140 1:3..434			TBX	AFUc13163				2.4E-38			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26352	ENU10147	ANI61S698:345..23			TBX	AFUc09912				5.7E-34			
26353	ENU10148	ANI61C11419:2373..1843			TBX	AFUc15881				1.6E-67			
26354	ENU10149	ANI61S2455:392..2			TBX	AFUc11066				1.1E-31			
26355	ENU10150	ANI61C3355:2104..2365			TBX	AFUc09161				2.7E-80			
26356	ENU10151	ANI61C3356:297..28			TBX	AFUc12958				1.1E-81			
26357	ENU10152	ANI61C4085:638..48			TBX	AFUc11270				1.1E-65			
26358	ENU10153	ANI61S2462:5..440			TBX	AFUc21510				3.8E-62			
26359	ENU10154	ANI61C3362:4..264			TBX	FGRc11478				4.6E-34			
26360	ENU10155	ANI61C3362:436..786			TBX	FGRc11478				4.6E-34			
26361	ENU10156	ANI61C11436:4996..4331			TBX	"AFUc04052, FGRc01908"				"7.1e-13, 4.3e-46"			
26362	ENU10157	ANI61C2646:3168..3605			TBX	AFUc14961				2.5E-47			
26363	ENU10158	ANI61C3377:959..459			TBX	AFUc22233				6.1E-41			
26364	ENU10159	ANI61C10717:4585..3701			TBX	AFUc11632				3.9E-65			
26365	ENU10160	ANI61C1929:584..5			TBX	AFUc13153				5.6E-52			

Table 6.6. Continued

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26366	ENU10161	ANI61C1072 5:528..16			TBX	AFUc12822				2.6E-35			
26367	ENU10162	ANI61C2662: 2551..2306			TBX	AFUc13641				5.8E-31			
26368	ENU10163	ANI61C3398: 387..870			TBX	AFUc18684				2E-44			
26369	ENU10164	ANI61C1146 2:3829..4053			TBX	AFUc13016				5.5E-42			
26370	ENU10165	ANI61C2676: 330..5			TBX	AFUc13919				6.5E-148			
26371	ENU10166	ANI61C2679: 1222..893			TBX	AFUc09698				2.1E-47			
26372	ENU10167	ANI61C1954: 679..9			TBX	"FGRc04985, Y13140"				"1.4e-62, 1.4e-35"			
26373	ENU10168	ANI61C2684: 71..694			TBX	AFUc06488				2.4E-82			
26374	ENU10169	ANI61C1075 3:1340..981			TBX	AFUc19770				9.7E-36			
26375	ENU10170	ANI61C1075 3:1723..1472			TBX	"AFUc17439, AFUc17439"				"2.2e-40, 6.0e-31"			
26376	ENU10171	ANI61C1076 2:980..528			TBX	AFUc10345				3.4E-32			
26377	ENU10172	ANI61C805:2 233..2634			TBX	AFUc15684				6.5E-95			
26378	ENU10173	ANI61C1077 1:216..4			TBX	AFUc14697				1.4E-103			
26379	ENU10174	ANI61C1077 6:3838..4329			TBX	AFUc21889				1.2E-40			

Gene annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26394	ENU10189	ANI61C9162:1393..776			TBX	AFUc14973				4.9E-32			
26395	ENU10190	ANI61C7710:775..35			TBX	AFUc12089				2.3E-64			
26396	ENU10191	ANI61C7715:3917..4234			TBX	FGRc09602				3.3E-33			
26397	ENU10192	ANI61C7717:6428..6108			TBX	FGRc18440				7.3E-33			
26398	ENU10193	ANI61C880:1600..692			TBX	AFUc05401				7E-61			
26399	ENU10194	ANI61C8450:2030..1656			TBX	AFUc14668				1.6E-40			
26400	ENU10195	ANI61C9184:31..390			TBX	AFUc08030				4.1E-49			
26401	ENU10196	ANI61C7728:1528..953			TBX	AFUc14112				1.2E-37			
26402	ENU10197	ANI61C8457:6314..5572			TBX	"AFUc09443, AFUc09443, FGRc19689, U00093"				"2.2e-54, 7.4e-41, 2.3e-26, 1.7e-34"			
26403	ENU10198	ANI61C8459:2032..1801			TBX	AFUc15223				2.5E-129			
26404	ENU10199	ANI61C8459:9064..8759			TBX	AFUc10030				3E-104			
26405	ENU10200	ANI61C893:2401..2670			TBX	AFUc14162				1.1E-84			
26406	ENU10201	ANI61C7735:754..1065			TBX	AFUc12028				5.3E-40			
26407	ENU10202	ANI61C8480:888..511			TBX	AFUc15553				3.6E-35			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26408	ENU10203	ANI61C8486:3..308			TBX	CALc04830				5.4E-77			
26409	ENU10204	ANI61C8494:3477..2449			TBX	AFUc14523				5E-90			
26410	ENU10205	ANI61C7767:1652..2095			TBX	AFUc05805				6.9E-138			
26411	ENU10206	ANI61C7776:1643..1987			TBX	AFUc10213				1.6E-33			
26412	ENU10207	ANI61S710:8..441			TBX	AFUc01898				7.8E-46			
26413	ENU10208	ANI61S34:6..293			TBX	AFUc09951				4.4E-40			
26414	ENU10209	ANI61S42:409..23			TBX	FGRc11175				1.1E-40			
26415	ENU10210	ANI61C4105:15..279			TBX	AFUc15131				2.2E-72			
26416	ENU10211	ANI61C4108:432..3			TBX	AFUc15554				3E-38			
26417	ENU10212	ANI61C3402:1678..1353			TBX	AFUc08075				2.3E-66			
26418	ENU10213	ANI61C4132:581..807			TBX	U00094				"9,4e-22"			
26419	ENU10214	ANI61C4132:1138..1458			TBX	AFUc01742				1.1E-35			
26420	ENU10215	ANI61C4132:3240..3479			TBX	FGRc07284				1.6E-95			
26421	ENU10216	ANI61C3412:711..1163			TBX	AFUc12614				9.6E-40			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26422	ENU10217	ANI61C4144:154..513			TBX	AFUc18185				3E-49			
26423	ENU10218	ANI61C4146:206..6			TBX	AFUc11980				2.7E-48			
26424	ENU10219	ANI61C3427:2300..2070			TBX	AFUc11170				1.1E-32			
26425	ENU10220	ANI61C4157:3987..3415			TBX	"AFUc22639, Y13135"				"1.5e-13, 3.2e-25"			
26426	ENU10221	ANI61C4160:27..296			TBX	AFUc20192				5.3E-35			
26427	ENU10222	ANI61C3443:512..24			TBX	AFUc17062				4.4E-47			
26428	ENU10223	ANI61C4182:2842..3151			TBX	Y13136				2.5e-18			
26429	ENU10224	ANI61C4192:4052..3765			TBX	AFUc14724				3.7E-90			
26430	ENU10225	ANI61C4194:2150..2505			TBX	AFUc11112				1E-37			
26431	ENU10226	ANI61C4195:809..1015			TBX	AFUc11252				5.6E-91			
26432	ENU10227	ANI61C4199:794..1340			TBX	"AFUc01489, AFUc19265"				"9.5e-48, 7.7e-08"			
26433	ENU10228	ANI61C3474:853..3			TBX	AFUc06878				3.1E-82			
26434	ENU10229	ANI61S2581:2..439			TBX	"AFUc18278, CALc04638"				"1.3e-25, 1.3e-31"			
26435	ENU10230	ANI61C3481:424..5			TBX	AFUc10462				1.5E-38			

Sequence description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26436	ENU10231	ANI61S1867:101..544			TBX	AFUc14374				1.7E-68			
26437	ENU10232	ANI61C2763:8..802			TBX	AFUc13692				5.8E-77			
26438	ENU10233	ANI61C2774:525..4			TBX	AFUc14947				1.7E-54			
26439	ENU10234	ANI61C10849:3248..3499			TBX	AFUc10042				4.5E-54			
26440	ENU10235	ANI61C10855:2191..2922			TBX	"AFUc08795, AFUc08853"				"6.4e-78, 1.6e-38"			
26441	ENU10236	ANI61C2798:939..448			TBX	AFUc04411				7.2E-31			
26442	ENU10237	ANI61C900:494..760			TBX	Z71256				9.0e-47			
26443	ENU10238	ANI61C904:1533..1126			TBX	CALc05922				2.2E-46			
26444	ENU10239	ANI61C9202:2010..1717			TBX	FGRc11250				2.3E-79			
26445	ENU10240	ANI61C10888:1767..1118			TBX	AFUc15937				5.5E-34			
26446	ENU10241	ANI61C9214:363..4			TBX	AFUc14249				2.9E-66			
26447	ENU10242	ANI61C9214:2824..2441			TBX	AFUc05949				1.8E-56			
26448	ENU10243	ANI61C10890:82..1020			TBX	"AFUc15972, AFUc15972"				"3.1e-67, 9.1e-74"			
26449	ENU10244	ANI61C10894:3385..2755			TBX	FGRc10423				9.6E-38			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26450	ENU10245	ANI61C9221:1982..2254			TBX	AFUc14012				2.7E-72			
26451	ENU10246	ANI61C936:1465..1980			TBX	AFUc15330				2.4E-132			
26452	ENU10247	ANI61C8502:769..171			TBX	"AFUc03429, AFUc18078"				"2.2e-09, 9.7e-43"			
26453	ENU10248	ANI61C945:2606..1959			TBX	AFUc13932				8.5E-51			
26454	ENU10249	ANI61C945:2854..2606			TBX	AFUc13932				8.5E-51			
26455	ENU10250	ANI61C8510:2200..1793			TBX	AFUc14805				2.3E-52			
26456	ENU10251	ANI61C8529:1547..2065			TBX	FGRc02575				1.3E-33			
26457	ENU10252	ANI61C8537:1088..33			TBX	FGRc10154				5.6E-44			
26458	ENU10253	ANI61C9268:4569..4189			TBX	AFUc20576				3.3E-49			
26459	ENU10254	ANI61C9269:1741..2743			TBX	"AFUc14083, AFUc15534"				"1.9e-19, 5.3e-32"			
26460	ENU10255	ANI61C7811:352..8			TBX	AFUc13321				1.9E-33			
26461	ENU10256	ANI61C9273:2..301			TBX	AFUc05348				2.6E-34			
26462	ENU10257	ANI61C9274:1360..1106			TBX	AFUc10007				9.1E-49			
26463	ENU10258	ANI61C989:1027..1779			TBX	AFUc15375				1.7E-71			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26478	ENU10273	ANI61C7865:1351..1782			TBX	AFUc06805				9E-55			
26479	ENU10274	ANI61C7870:2395..2601			TBX	AFUc12018				1.4E-76			
26480	ENU10275	ANI61C7885:1235..826			TBX	"AFUc00688, AFUc00688"				"2.4e-51, 9.0e-51"			
26481	ENU10276	ANI61C7896:72..566			TBX	AFUc18887				6.5E-44			
26482	ENU10277	ANI61S822:621..386			TBX	"AFUc14236, AFUc14236"				"1.2e-34, 5.1e-39"			
26483	ENU10278	ANI61S3327:45..308			TBX	AFUc15972				2.1E-42			
26484	ENU10279	ANI61C4225:2091..1639			TBX	AFUc15269				7.6E-52			
26485	ENU10280	ANI61C4226:375..13			TBX	Y13137				8.5e-18			
26486	ENU10281	ANI61S853:424..20			TBX	AFUc13855				5.5E-40			
26487	ENU10282	ANI61C4239:596..2			TBX	FGRc11037				4.9E-32			
26488	ENU10283	ANI61C4242:3202..3477			TBX	AFUc14037				5.5E-67			
26489	ENU10284	ANI61C4262:113..679			TBX	AFUc08092				1.8E-56			
26490	ENU10285	ANI61C4263:377..6			TBX	AFUc01021				2E-52			
26491	ENU10286	ANI61C2812:3..762			TBX	"AFUc01646, AFUc11287"				"2.1e-33, 3.4e-46"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26492	ENU10287	ANI61C4270: 4242..4855			TBX	AFUc02593				2.2E-34			
26493	ENU10288	ANI61C3544: 3554..3094			TBX	AFUc12369				1.4E-40			
26494	ENU10289	ANI61C2817: 373..15			TBX	AFUc15017				1.3E-45			
26495	ENU10290	ANI61C3548: 1461..1129			TBX	FGRc26479				2.3E-41			
26496	ENU10291	ANI61S1939: 606..169			TBX	AFUc13323				3.7E-38			
26497	ENU10292	ANI61C3566: 4239..4448			TBX	Y13136				1.4e-52			
26498	ENU10293	ANI61C1090 0:536..907			TBX	FGRc11747				9.5E-32			
26499	ENU10294	ANI61C3588: 2278..2856			TBX	AFUc13885				2.5E-56			
26500	ENU10295	ANI61C3592: 358..8			TBX	AFUc09097				5.2E-32			
26501	ENU10296	ANI61C1093 2:1213..582			TBX	AFUc15923				1.3E-49			
26502	ENU10297	ANI61C1093 6:2207..1787			TBX	AFUc05492				5.8E-53			
26503	ENU10298	ANI61C1093 7:782..1237			TBX	AFUc14290				2.1E-41			
26504	ENU10299	ANI61C1094 3:423..671			TBX	AFUc17390				6.5E-42			
26505	ENU10300	ANI61C2880: 800..504			TBX	AFUc16447				1.2E-32			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	Description
26506	ENU10301	ANI61C2882: 808..1305			TBX	AFUc13856				2.1E-47			
26507	ENU10302	ANI61C2885: 481..783			TBX	AFUc14906				7.3E-35			
26508	ENU10303	ANI61C1096 3:4720..4947			TBX	AFUc01385				2.5E-37			
26509	ENU10304	ANI61C1097 4:6..680			TBX	AFUc09332				2E-40			
26510	ENU10305	ANI61C1097 8:377..102			TBX	AFUc10468				8E-37			
26511	ENU10306	ANI61C9300: 2401..1704			TBX	"AFUc05781, AFUc12769"				"2.7e-47, 2.6e-47"			
26512	ENU10307	ANI61C1098 7:2320..2655			TBX	AFUc21995				2.4E-46			
26513	ENU10308	ANI61C1098 9:469..18			TBX	AFUc12150				4.4E-39			
26514	ENU10309	ANI61C9310: 741..25			TBX	AFUc15016				4E-81			
26515	ENU10310	ANI61C9318: 4838..4473			TBX	AFUc07003				7.7E-89			
26516	ENU10311	ANI61C9326: 1564..1956			TBX	AFUc15104				4.7E-65			
26517	ENU10312	ANI61C8605: 1497..625			TBX	AFUc06416				5.3E-44			
26518	ENU10313	ANI61C8608: 3240..2755			TBX	AFUc04235				4.7E-50			
26519	ENU10314	ANI61C8608: 4091..3681			TBX	AFUc01064				3.8E-53			

Gene Organization

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26520	ENU10315	ANI61C8615: 3641..3897			TBX	AFUc15221				3.5E-54			
26521	ENU10316	ANI61C9345: 302..3			TBX	AFUc15332				3E-33			
26522	ENU10317	ANI61C8618: 2899..2618			TBX	AFUc15281				1.8E-47			
26523	ENU10318	ANI61C8618: 3589..3119			TBX	AFUc03740				8.5E-36			
26524	ENU10319	ANI61C9355: 543..7			TBX	AFUc15687				9.2E-108			
26525	ENU10320	ANI61C9362: 1959..1529			TBX	AFUc21030				1.2E-35			
26526	ENU10321	ANI61C9363: 1339..866			TBX	AFUc20167				2.7E-42			
26527	ENU10322	ANI61C8635: 1402..1717			TBX	AFUc15942				3.1E-34			
26528	ENU10323	ANI61C9369: 2437..1592			TBX	"AFUc01185, FGRC20865"				"6.1e-20, 2.0e-37"			
26529	ENU10324	ANI61C9377: 955..1296			TBX	AFUc08600				4.6E-38			
26530	ENU10325	ANI61C8649: 3568..3825			TBX	"AFUc09782, FGRC24890"				"2.0e-21, 1.9e-43"			
26531	ENU10326	ANI61C8653: 2070..2574			TBX	AFUc04641				8.6E-43			
26532	ENU10327	ANI61C8656: 2089..2426			TBX	T18724				1.7e-22			
26533	ENU10328	ANI61C9386: 650..2094			TBX	AFUc13410				8.1E-94			

GenBank Consistent

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrq	Description
26534	ENU10329	ANI61C8659: 566..294			TBX	AFUc10787				2.7E-74			
26535	ENU10330	ANI61C7939: 1440..1162			TBX	AFUc11560				5.5E-57			
26536	ENU10331	ANI61C8669: 4081..4653			TBX	AFUc05795				9E-47			
26537	ENU10332	ANI61C8672: 12..1160			TBX	AFUc13321				2.5E-89			
26538	ENU10333	ANI61C8685: 144..353			TBX	AFUc13122				2.1E-67			
26539	ENU10334	ANI61C7963: 2540..3006			TBX	AFUc09860				1.6E-37			
26540	ENU10335	ANI61C7988: 556..248			TBX	AFUc03753				7.1E-40			
26541	ENU10336	ANI61C7994: 2406..3131			TBX	AFUc02330				3.1E-48			
26542	ENU10337	ANI61C5025: 1520..773			TBX	AFUc08324				5.2E-49			
26543	ENU10338	ANI61C4311: 338..670			TBX	AFUc03634				4.4E-34			
26544	ENU10339	ANI61C5041: 132..716			TBX	AFUc05209				5.7E-57			
26545	ENU10340	ANI61C4315: 2667..2467			TBX	AFUc14948				4.4E-68			
26546	ENU10341	ANI61C5049: 1100..303			TBX	AFUc02784				4.9E-52			
26547	ENU10342	ANI61C5053: 7..360			TBX	AFUc12855				1.4E-81			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26548	ENU10343	ANI61C3616:1021..686			TBX	AFUc11581				2E-31			
26549	ENU10344	ANI61C5075:958..1185			TBX	AFUc14875				2.5E-141			
26550	ENU10345	ANI61C4346:343..761			TBX	AFUc04097				3.4E-34			
26551	ENU10346	ANI61C3623:1889..2795			TBX	"AFUc11914, FGRC09621"				"1.9e-72, 9.4e-31"			
26552	ENU10347	ANI61C3623:400..8			TBX	AFUc15572				3.6E-44			
26553	ENU10348	ANI61C4360:1029..1415			TBX	AFUc15474				1.7E-128			
26554	ENU10349	ANI61C3634:888..1166			TBX	AFUc14338				1.6E-116			
26555	ENU10350	ANI61C5094:8..361			TBX	AFUc08772				6.5E-38			
26556	ENU10351	ANI61C3637:2145..1699			TBX	AFUc09606				5E-40			
26557	ENU10352	ANI61C2915:2915..2528			TBX	AFUc11110				5.6E-35			
26558	ENU10353	ANI61C4374:2149..2712			TBX	Z71256				1.4e-56			
26559	ENU10354	ANI61C3652:2..604			TBX	AFUc00801				3.7E-35			
26560	ENU10355	ANI61C2931:8..617			TBX	AFUc08105				1.6E-51			
26561	ENU10356	ANI61C3670:923..1135			TBX	AFUc11895				3.5E-39			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	% Description
26562	ENU10357	ANI61C3672: 455..679			TBX	AFUc15435				6.4E-78			
26563	ENU10358	ANI61C2949: 167..850			TBX	AFUc07056				1.8E-49			
26564	ENU10359	ANI61S2794: 559..104			TBX	AFUc10264				8.5E-70			
26565	ENU10360	ANI61C2968: 1521..2163			TBX	AFUc05625				1E-67			
26566	ENU10361	ANI61C2976: 1861..2472			TBX	AFUc13072				1.6E-80			
26567	ENU10362	ANI61C2982: 515..10			TBX	AFUc08724				5.7E-34			
26568	ENU10363	ANI61C9433: 998..517			TBX	AFUc03107				2.7E-42			
26569	ENU10364	ANI61C9435: 444..31			TBX	AFUc08363				3.8E-34			
26570	ENU10365	ANI61C9442: 3306..2878			TBX	AFUc14805				2E-54			
26571	ENU10366	ANI61C8715: 442..867			TBX	AFUc05950				5.3E-55			
26572	ENU10367	ANI61C8716: 1384..1013			TBX	AFUc14901				3.1E-33			
26573	ENU10368	ANI61C9454: 2260..1922			TBX	AFUc15792				5.4E-55			
26574	ENU10369	ANI61C8731: 1663..2388			TBX	AFUc06663				3.6E-38			
26575	ENU10370	ANI61C8733: 1307..567			TBX	AFUc14363				2E-135			

Accession Description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Prob	% id	cvr	Description
26590	ENU10385	ANI61C5150: 717..1240			TBX	"AFUc01789, AFUc17092"			"5.8e-31, 7.6e-11"			
26591	ENU10386	ANI61C4423: 1282..1818			TBX	AFUc14561			7.7E-32			
26592	ENU10387	ANI61C5159: 698..164			TBX	AFUc08493			9.8E-49			
26593	ENU10388	ANI61C3704: 361..854			TBX	AFUc07782			5.3E-83			
26594	ENU10389	ANI61C4437: 1727..2095			TBX	AFUc10065			7.2E-31			
26595	ENU10390	ANI61C5173: 1175..777			TBX	AFUc15520			3E-125			
26596	ENU10391	ANI61C3725: 729..1112			TBX	AFUc01619			1.6E-47			
26597	ENU10392	ANI61C3734: 34..558			TBX	AFUc16279			7.1E-47			
26598	ENU10393	ANI61C3735: 2099..3050			TBX	AFUc12357			7.2E-77			
26599	ENU10394	ANI61C4464: 433..2			TBX	AFUc07536			1.6E-37			
26600	ENU10395	ANI61C3736: 3424..3224			TBX	AFUc06687			8.9E-35			
26601	ENU10396	ANI61C3737: 281..3			TBX	AFUc09976			1.8E-68			
26602	ENU10397	ANI61C3743: 627..92			TBX	AFUc16169			3.2E-41			
26603	ENU10398	ANI61C3747: 860..1082			TBX	AFUc14515			1.4E-45			

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26618	ENU10413	ANI61C9577: 5153..5725			TBX	AFUc20879				2.9E-58			
26619	ENU10414	ANI61C9579: 2165..1657			TBX	"AFUc13295, FGRc06579"				"5.7e-31, 1.5e-12"			
26620	ENU10415	ANI61C9585: 845..213			TBX	AFUc11738				6.2E-96			
26621	ENU10416	ANI61C8873: 1147..668			TBX	AFUc04140				1.4E-46			
26622	ENU10417	ANI61C8876: 126..374			TBX	Y13135				1.9e-146			
26623	ENU10418	ANI61C8878: 4257..3709			TBX	AFUc15197				1.1E-100			
26624	ENU10419	ANI61C5200: 1392..2379			TBX	"CALc06185, CALc06185"				"4.1e-37, 5.6e-13"			
26625	ENU10420	ANI61C5207: 48..260			TBX	AFUc15608				1.5E-46			
26626	ENU10421	ANI61C5211: 2..232			TBX	AFUc09688				2.8E-32			
26627	ENU10422	ANI61C5228: 44..370			TBX	AFUc14750				1.2E-90			
26628	ENU10423	ANI61C5238: 983..675			TBX	AFUc13449				1.1E-42			
26629	ENU10424	ANI61C5238: 1776..1549			TBX	AFUc13449				1.1E-42			
26630	ENU10425	ANI61C5240: 938..63			TBX	AFUc14032				1E-65			
26631	ENU10426	ANI61C4514: 588..343			TBX	AFUc08117				2.6E-31			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrq	Description
26646	ENU10441	ANI61C4587: 401..2			TBX	FGRc06237				2.7E-37			
26647	ENU10442	ANI61C3885: 720..1126			TBX	"AFUc05920, AFUc05920"				"1.6e-31, 7.0e-60"			
26648	ENU10443	ANI61C3890: 1104..649			TBX	AFUc09816				4.1E-48			
26649	ENU10444	ANI61C9618: 2..465			TBX	AFUc03874				7.4E-63			
26650	ENU10445	ANI61C9634: 5066..4527			TBX	AFUc02404				4.9E-39			
26651	ENU10446	ANI61C9636: 4726..4224			TBX	"FGRc17533, Y13140"				"4.0e-28, 2.3e-26"			
26652	ENU10447	ANI61C9637: 1073..178			TBX	FGRc10589				4.6E-75			
26653	ENU10448	ANI61C8908: 2362..2835			TBX	AFUc15919				3E-49			
26654	ENU10449	ANI61C8910: 391..2			TBX	AFUc04556				3.7E-43			
26655	ENU10450	ANI61C8913: 3476..3057			TBX	AFUc03973				1.5E-35			
26656	ENU10451	ANI61C9642: 1286..852			TBX	FGRc10508				2.7E-48			
26657	ENU10452	ANI61C8921: 2219..2962			TBX	AFUc13687				2.4E-34			
26658	ENU10453	ANI61C8921: 5235..4886			TBX	AFUc08999				3.6E-32			
26659	ENU10454	ANI61C9656: 2345..2824			TBX	AFUc12498				6.1E-46			

66666" description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26660	ENU10455	ANI61C8932: 646..5			TBX	FGRc06110				9.2E-38			
26661	ENU10456	ANI61C9663: 4438..3729			TBX	AFUc11984				1.2E-63			
26662	ENU10457	ANI61C8941: 837..1202			TBX	AFUc07937				1.5E-56			
26663	ENU10458	ANI61C9673: 3351..2389			TBX	"FGRc06761, FGRc13645"				"4.5e-12, 1.3e-33"			
26664	ENU10459	ANI61C9683: 1130..903			TBX	AFUc14283				1.4E-60			
26665	ENU10460	ANI61C8956: 3704..3153			TBX	AFUc04448				6.7E-60			
26666	ENU10461	ANI61C8958: 282..31			TBX	AFUc03959				2.9E-47			
26667	ENU10462	ANI61C8958: 512..282			TBX	AFUc03959				2.9E-47			
26668	ENU10463	ANI61C8962: 3300..3755			TBX	FGRc11722				2.7E-50			
26669	ENU10464	ANI61C8966: 3485..4861			TBX	AFUc12092				1.2E-83			
26670	ENU10465	ANI61C9697: 3970..3734			TBX	FGRc02733				1.1E-33			
26671	ENU10466	ANI61C9698: 1565..1311			TBX	AFUc09469				6.9E-86			
26672	ENU10467	ANI61C8971: 25..270			TBX	AFUc19130				1.8E-35			
26673	ENU10468	ANI61C8975: 606..31			TBX	AFUc10229				5.8E-58			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26688	ENU10483	ANI61C5339:1771..1418			TBX	AFUc18220				1.3E-41			
26689	ENU10484	ANI61C5346:1293..1616			TBX	AFUc11752				5.5E-32			
26690	ENU10485	ANI61C3905:1127..333			TBX	AFUc02952				2.5E-70			
26691	ENU10486	ANI61C3905:1507..1292			TBX	AFUc13396				3.6E-53			
26692	ENU10487	ANI61C6092:510..307			TBX	AFUc15283				8.6E-35			
26693	ENU10488	ANI61C3908:1013..1393			TBX	AFUc09536				6.1E-57			
26694	ENU10489	ANI61C3916:1331..1672			TBX	AFUc14010				1.5E-102			
26695	ENU10490	ANI61C3922:3..212			TBX	AFUc15201				3.9E-38			
26696	ENU10491	ANI61S3768:482..240			TBX	AFUc08524				9.3E-35			
26697	ENU10492	ANI61C4662:613..335			TBX	AFUc13777				2.1E-40			
26698	ENU10493	ANI61C4670:745..53			TBX	AFUc12006				1.8E-56			
26699	ENU10494	ANI61C3958:1367..1068			TBX	U00093				4.9e-16			
26700	ENU10495	ANI61C3964:5879..6301			TBX	AFUc17957				8.5E-32			
26701	ENU10496	ANI61C3979:1132..3123			TBX	AFUc15917				3.1E-152			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr g	Description
26702	ENU10497	ANI61C1002: 2691..3661			TBX	AFUc11715				9E-91			
26703	ENU10498	ANI61C1002: 2096..1689			TBX	AFUc03394				3.1E-34			
26704	ENU10499	ANI61C3982: 934..1254			TBX	AFUc15781				9.6E-174			
26705	ENU10500	ANI61C1030: 2411..3198			TBX	AFUc10447				2.7E-51			
26706	ENU10501	ANI61C9702: 4068..4367			TBX	"AFUc10199, AFUc10199"				"1.4e-80, 6.8e-74"			
26707	ENU10502	ANI61C1072: 754..13			TBX	AFUc15759				4.6E-43			
26708	ENU10503	ANI61C9726: 653..1			TBX	CALc05491				6.1E-33			
26709	ENU10504	ANI61C9729: 2216..1656			TBX	AFUc14102				5.2E-39			
26710	ENU10505	ANI61C9737: 343..26			TBX	AFUc14470				6.8E-75			
26711	ENU10506	ANI61C9737: 1274..918			TBX	AFUc14470				6.8E-75			
26712	ENU10507	ANI61C9768: 1271..2131			TBX	U00094				3.0e-246			
26713	ENU10508	ANI61C9771: 4119..4642			TBX	AFUc07319				3.7E-53			
26714	ENU10509	ANI61C9776: 5848..5597			TBX	AFUc10732				1.6E-49			
26715	ENU10510	ANI61C9779: 777..364			TBX	Y13137				5.8e-80			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26716	ENU10511	ANI61C9783: 253..3			TBX	AFUc13340				1.2E-31			
26717	ENU10512	ANI61C9791: 7939..7275			TBX	AFUc11371				4.4E-76			
26718	ENU10513	ANI61C9793: 14..865			TBX	AFUc07854				1.4E-78			
26719	ENU10514	ANI61C6117: 1129..1617			TBX	AFUc09532				2.1E-48			
26720	ENU10515	ANI61S4503: 575..17			TBX	AFUc08015				3.8E-77			
26721	ENU10516	ANI61C5405: 352..44			TBX	AFUc04307				6.2E-38			
26722	ENU10517	ANI61C6134: 666..878			TBX	AFUc12780				4.1E-49			
26723	ENU10518	ANI61C6136: 2170..2385			TBX	AFUc12645				8.3E-105			
26724	ENU10519	ANI61C6143: 352..5			TBX	FGRc15010				5.3E-33			
26725	ENU10520	ANI61C5422: 209..562			TBX	FGRc06384				1.1E-40			
26726	ENU10521	ANI61C4701: 321..94			TBX	AFUc05559				3.7E-89			
26727	ENU10522	ANI61C6167: 85..837			TBX	AFUc14614				1.4E-83			
26728	ENU10523	ANI61C6169: 533..844			TBX	AFUc15069				1.2E-59			
26729	ENU10524	ANI61C4711: 804..5			TBX	AFUc12529				1.2E-107			

[illegible]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26730	ENU10525	ANI61C4714:1635..1198			TBX	AFUc11891				3.4E-32			
26731	ENU10526	ANI61C4721:76..363			TBX	AFUc07768				1.4E-58			
26732	ENU10527	ANI61C6180:963..1289			TBX	AFUc18477				7.1E-38			
26733	ENU10528	ANI61C4733:77..687			TBX	AFUc13638				1E-38			
26734	ENU10529	ANI61C5462:921..253			TBX	AFUc14210				6.7E-68			
26735	ENU10530	ANI61C5471:621..1014			TBX	AFUc14562				3.3E-44			
26736	ENU10531	ANI61C4749:1693..1490			TBX	AFUc15821				1.7E-128			
26737	ENU10532	ANI61S4583:51..377			TBX	AFUc15972				1.6E-33			
26738	ENU10533	ANI61C4764:494..195			TBX	AFUc11693				1.4E-103			
26739	ENU10534	ANI61C4784:1322..855			TBX	AFUc00822				1.2E-52			
26740	ENU10535	ANI61C4790:720..457			TBX	AFUc00901				5.3E-36			
26741	ENU10536	ANI61C4796:1558..2298			TBX	AFUc15050				3E-86			
26742	ENU10537	ANI61C1104:1273..611			TBX	CALc06186				8E-40			
26743	ENU10538	ANI61C1112:2794..1976			TBX	AFUc11351				5.1E-46			

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26744	ENU10539	ANI61C1120:12513..12740			TBX	CALc03518				2.3E-56			
26745	ENU10540	ANI61C1120:1790..1437			TBX	AFUc15689				1.1E-41			
26746	ENU10541	ANI61C1127:2014..1043			TBX	AFUc11947				1E-105			
26747	ENU10542	ANI61C1135:1766..2113			TBX	AFUc15916				3.1E-98			
26748	ENU10543	ANI61C1137:10..315			TBX	AFUc15972				1.2E-120			
26749	ENU10544	ANI61C1137:430..1264			TBX	AFUc15972				1.2E-120			
26750	ENU10545	ANI61C1138:193..701			TBX	AFUc15803				6.3E-91			
26751	ENU10546	ANI61C1138:1603..1989			TBX	AFUc15803				6.3E-91			
26752	ENU10547	ANI61C1139:5367..5110			TBX	CALc06190				8.4E-44			
26753	ENU10548	ANI61C1141:2040..2351			TBX	AFUc22467				1.9E-71			
26754	ENU10549	ANI61C9807:2386..2132			TBX	AFUc13156				3.2E-40			
26755	ENU10550	ANI61C1183:3285..3707			TBX	AFUc16697				9.8E-57			
26756	ENU10551	ANI61C1188:2..371			TBX	AFUc15915				8.4E-80			
26757	ENU10552	ANI61C1188:4690..4926			TBX	AFUc15848				2.9E-120			

Gene annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26758	ENU10553	ANI61C1188: 7009..7704			TBX	AFUc13465				2.6E-50			
26759	ENU10554	ANI61C9827: 4904..4662			TBX	AFUc01941				4.4E-33			
26760	ENU10555	ANI61C1190: 1669..1460			TBX	AFUc19119				3.3E-46			
26761	ENU10556	ANI61C9876: 4899..5639			TBX	AFUc01111				4.6E-51			
26762	ENU10557	ANI61C9878: 1670..1978			TBX	FGRc13922				3.2E-51			
26763	ENU10558	ANI61C9880: 4442..4932			TBX	AFUc19094				8.2E-36			
26764	ENU10559	ANI61C9880: 5038..5410			TBX	AFUc10800				2.7E-74			
26765	ENU10560	ANI61C9880: 1147..719			TBX	AFUc20412				4.8E-39			
26766	ENU10561	ANI61C9882: 5925..6479			TBX	AFUc10536				1.3E-48			
26767	ENU10562	ANI61C9883: 1765..2013			TBX	AFUc03896				9.4E-34			
26768	ENU10563	ANI61C6208: 4005..4583			TBX	AFUc02427				6.4E-42			
26769	ENU10564	ANI61C6220: 228..691			TBX	AFUc13617				7.9E-152			
26770	ENU10565	ANI61S4601: 369..16			TBX	AFUc17622				9.7E-46			
26771	ENU10566	ANI61C5501: 1905..2144			TBX	CALc02466				3.2E-69			

Geneious

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26772	ENU10567	ANI61C5504: 719..1018			TBX	AFUc13011				2.1E-57			
26773	ENU10568	ANI61C5512: 1004..735			TBX	AFUc15725				3.5E-35			
26774	ENU10569	ANI61C5520: 795..3			TBX	AFUc14374				2.6E-96			
26775	ENU10570	ANI61C5524: 479..9			TBX	AFUc05656				7.3E-37			
26776	ENU10571	ANI61C6258: 2595..1909			TBX	AFUc12895				9.4E-66			
26777	ENU10572	ANI61C6260: 36..472			TBX	AFUc12576				4.9E-31			
26778	ENU10573	ANI61C5533: 2815..3542			TBX	Y13134				1.1e-52			
26779	ENU10574	ANI61C4808: 1828..2380			TBX	"AFUc14618, FGRc25347"				"5.2e-76, 1.6e-18"			
26780	ENU10575	ANI61C5543: 286..621			TBX	AFUc17116				3.3E-51			
26781	ENU10576	ANI61C6279: 992..1635			TBX	AFUc10520				3.2E-62			
26782	ENU10577	ANI61C4820: 1166..402			TBX	AFUc12278				1.3E-52			
26783	ENU10578	ANI61C4825: 3..263			TBX	AFUc09182				2.7E-118			
26784	ENU10579	ANI61C4829: 541..759			TBX	AFUc02495				3.4E-45			
26785	ENU10580	ANI61C6294: 245..3			TBX	AFUc05031				1.9E-36			

Table 3. Continued

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26786	ENU10581	ANI61C6299: 603..1086			TBX	AFUc13847				2.2E-59			
26787	ENU10582	ANI61S3944: 5..361			TBX	AFUc14576				2.3E-41			
26788	ENU10583	ANI61C4841: 161..523			TBX	AFUc11703				7.1E-59			
26789	ENU10584	ANI61C4844: 1224..514			TBX	AFUc14922				1.1E-58			
26790	ENU10585	ANI61C5574: 4287..4858			TBX	AFUc12427				3.3E-48			
26791	ENU10586	ANI61C4851: 1359..1936			TBX	AFUc15187				6.8E-127			
26792	ENU10587	ANI61C4852: 465..217			TBX	AFUc11440				2.2E-64			
26793	ENU10588	ANI61C4858: 4225..3968			TBX	AFUc18745				6.1E-58			
26794	ENU10589	ANI61C1213: 666..2015			TBX	"AFUc00755, AFUc11547, AFUc21642"				"7.2e-48, 3.7e-60, 5.5e-50"			
26795	ENU10590	ANI61C1002 1:2042..2257			TBX	Y13137				1.7e-114			
26796	ENU10591	ANI61C1002 1:2807..3483			TBX	Y13137				1.7e-114			
26797	ENU10592	ANI61C1002 1:5043..5705			TBX	Y13137				1.7e-114			
26798	ENU10593	ANI61C1233: 104..469			TBX	AFUc15972				3E-223			
26799	ENU10594	ANI61C1233: 593..2227			TBX	"AFUc15972, AFUc15972"				"2.5e-220, 3.0e-223"			

[illegible]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr g	Description
26810	ENU10605	ANI61C7328: 5293..6820	2	1	GSP								
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			-	2									
			5	9									
			0	-									
				1									
26811	ENU10606	ANI61C1031 8:4988..5776		4	GSP								
				5									
26812	ENU10607	ANI61C6288: 9175..4851	2	7	GSP								
			7	5									
			-	2									
			5	-									
			0	7									
				7									
26812	ENU10607	ANI61C6288: 9175..4851		9	GSP								
			2	2									
			5	2									
			-	7									
			5	8									
			0	-									
26812	ENU10607	ANI61C6288: 9175..4851		2	GSP								
				3									
				0									
				7									

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26813	ENU10608	ANI61C1025: 943..2449	2	1	GSP								
			5	4									
			-	1									
			4	5									
			4	-									
			1	1									
			4	4									
			3	3									
26814	ENU10609	ANI50C8686 _1:101..1327	2	1	GSP								
			5	1									
			-	9									
			4	1									
			6	-									
			1	1									
			2	2									
			0	0									
26815	ENU10610	ANI61C8855: 1121..3430	9	9	GSP								
			2	1									
			5	9									
			-	6									
			4	8									
			7	-									
			1	1									
			9	9									
			9	9									
			5	5									

Genomic Annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26816	ENU10611	ANI61C4238:1653..2569			GSP								
26817	ENU10612	ANI61C9758:5232..2829			GSP								
26818	ENU10613	ANI61C9777:4913..3682			GSP								

Genomic Coordinates

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26819	ENU10614	ANT61C9272:2805..4329			GSP								
26820	ENU10615	ANT61C11205:3505..5508			GSP								
26821	ENU10616	ANT61C11368:3956..3354			GSP								
26822	ENU10617	ANT61C3922:221..1201			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr%	Description
26823	ENU10618	ANT61C4244:1752..25			GSP								
26824	ENU10619	ANT61C9662:1762..3272			GSP								
26825	ENU10620	ANT61C1189:733..2186			GSP								

Gene annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr%	Description
26826	ENU10621	ANI61C852:1			GSP								
		055..1534											
26827	ENU10622	ANI61C1018			GSP								
		8:2524..1832											
26828	ENU10623	ANI61C1106			GSP								
		4:4467..5468											
26829	ENU10624	ANI61C1037			GSP								
		9:2558..3166											

Genes in Genes

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26830	ENU10625	ANI61C8159:1418..708			GSP								
26831	ENU10626	ANI61C4204:4458..1758			GSP								
26832	ENU10627	ANI61C9269:447..1520			GSP								

Contig coverage

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26833	ENU10628	ANI61C1174: 4..927			GSP								

26834	ENU10629	ANI61C1099 8:6512..4967			GSP								
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26835	ENU10630	ANI61C3343: 3012..1656			GSP								
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Gene Annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26836	ENU10631	ANI61C1023 6:138..1026			GSP								
26837	ENU10632	ANI61C9178: 4154..3195			GSP								
26838	ENU10633	ANI61C8787: 2798..117			GSP								
26839	ENU10634	ANI61C1052 2:9..1581			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26840	ENU10635	ANI61C391:1 157..2307			GSP								
26841	ENU10636	ANI61C8594: 354..1610			GSP								
26842	ENU10637	ANI61C5881: 796..2073			GSP								

Genomic Data

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr	% Description
26843	ENU10638	ANI61C1067 6:1673..506			GSP								
26844	ENU10639	ANI61C1026 6:639..1493			GSP								
26845	ENU10640	ANI61C9273: 2356..3502			GSP								
26846	ENU10641	ANI61C9135: 1310..282			GSP								

Gene annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26847	ENU10642	ANI61C4057:12..1370			GSP								
26848	ENU10643	ANI61C5181:205..730			GSP								
26849	ENU10644	ANI61C5163:1648..925			GSP								
26850	ENU10645	ANI61C9611:1060..208			GSP								

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr%	Description
26851	ENU10646	ANI61C6211:5848..3572			GSP								
26852	ENU10647	ANI61C3390:1827..500			GSP								
26853	ENU10648	ANI61C405:2513..1849			GSP								
26854	ENU10649	ANI61C8967:1333..2100			GSP								

GenBank accession

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr%	Description
26855	ENU10650	ANI61C6915; 231..1067			GSP								
26856	ENU10651	ANI61C9116; 4511..5203			GSP								
26857	ENU10652	ANI61C2197; 153..952			GSP								
26858	ENU10653	ANI61C1026 9:343..52			GSP								
26859	ENU10654	ANI61C309:1 624..2155			GSP								
26860	ENU10655	ANI61C1027 9:3325..3609			GSP								
26861	ENU10656	ANI61C1480; 944..27			GSP								
26862	ENU10657	ANI61C1029 5:2764..2435			GSP								
26863	ENU10658	ANI61C7211; 1755..1192			GSP								
26864	ENU10659	ANI61C7220; 1287..1690			GSP								

66660 = 66660

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr g	Description
26877	ENU10672	ANI61C6599:2219..1887			GSP								
26878	ENU10673	ANI61S277:141..353			GSP								
26879	ENU10674	ANI61C11067:3583..3283	2	3	GSP								
			5	9									
			-	4									
			4	-									
			6	4									
				1									
				7									
26880	ENU10675	ANI61C2213:588..10			GSP								
26881	ENU10676	ANI61C2215:7849..7241			GSP								
26882	ENU10677	ANI61C2223:191..631			GSP								
26883	ENU10678	ANI61C2224:498..845			GSP								
26884	ENU10679	ANI61C2229:298..57			GSP								
26885	ENU10680	ANI61C11020:275..40			GSP								
26886	ENU10681	ANI61C1505:482..971			GSP								
26887	ENU10682	ANI61C10300:973..1299			GSP								
26888	ENU10683	ANI61C11036:2132..1698			GSP								

GenBank Submission

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26903	ENU10698	ANI61C1036 1:6952..7162			GSP								
26904	ENU10699	ANI61C1036 3:3081..2758			GSP								
26905	ENU10700	ANI61C1109 8:804..166			GSP								
26906	ENU10701	ANI61C425:6 27..833			GSP								
26907	ENU10702	ANI61C8007: 408..139			GSP								
26908	ENU10703	ANI61C7305: 1365..2019			GSP								
26909	ENU10704	ANI61C7309: 528..756			GSP								
26910	ENU10705	ANI61C474:3 7..324			GSP								
26911	ENU10706	ANI61C7312: 392..165			GSP								
26912	ENU10707	ANI61C485:5 84..121			GSP								
26913	ENU10708	ANI61C6606: 379..762			GSP								
26914	ENU10709	ANI61C8075: 1744..2038			GSP								
26915	ENU10710	ANI61C8086: 1038..1379			GSP								
26916	ENU10711	ANI61C7373: 531..97			GSP								

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26928	ENU10723	ANI61C2339:4593..5853			GSP								
26929	ENU10724	ANI61S1445:217..447			GSP								
26930	ENU10725	ANI61C7400:2503..1237			GSP								
26931	ENU10726	ANI61C3077:672..14			GSP								
26932	ENU10727	ANI61C10411:563..261			GSP								
26933	ENU10728	ANI61S1452:359..18			GSP								
26934	ENU10729	ANI61C2352:176..792			GSP								
26935	ENU10730	ANI61S1463:286..74			GSP								
26936	ENU10731	ANI61C2361:934..60			GSP								
26937	ENU10732	ANI61C2361:3052..3372			GSP								
26938	ENU10733	ANI61C11165:1645..2411			GSP								

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr%	Description
26939	ENU10734	ANI61C2372:855..1133			GSP								
26940	ENU10735	ANI61C2372:1652..2011			GSP								
26941	ENU10736	ANI61C10454:4570..4971			GSP								
26942	ENU10737	ANI61C1661:882..424			GSP								
26943	ENU10738	ANI61C10474:160..561			GSP								
26944	ENU10739	ANI61C10475:353..12			GSP								
26945	ENU10740	ANI61C1686:634..265			GSP								
26946	ENU10741	ANI61C511:32..511			GSP								
26947	ENU10742	ANI61C511:955..2004			GSP								
26948	ENU10743	ANI61C515:507..1530			GSP								
26949	ENU10744	ANI61C517:636..10			GSP								
26950	ENU10745	ANI61C1697:907..698			GSP								
26951	ENU10746	ANI61C531:313..1072			GSP								
26952	ENU10747	ANI61C534:322..579			GSP								

[illegible]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26965	ENU10760	ANI61C6736:2119..302			GSP								
26966	ENU10761	ANI61C8198:666..154			GSP								
26967	ENU10762	ANI61C6749:318..664			GSP								
26968	ENU10763	ANI61C7495:1744..2273			GSP								
26969	ENU10764	ANI61C6784:866..1216			GSP								
26970	ENU10765	ANI61C6791:598..892			GSP								
26971	ENU10766	ANI61S465:199..480			GSP								
26972	ENU10767	ANI61C3116:2211..1954			GSP								
26973	ENU10768	ANI61S2221:292...5			GSP								
26974	ENU10769	ANI61C4578:2006..79			GSP								
26975	ENU10770	ANI61C2435:4559..4236			GSP								

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26990	ENU10785	ANI61C1057 5:1238..939			GSP								
26991	ENU10786	ANI61C1057 6:1519..1313			GSP								
26992	ENU10787	ANI61C1780: 503..74			GSP								
26993	ENU10788	ANI61C1780: 2749..3104			GSP								
26994	ENU10789	ANI61C1790: 326..98			GSP								
26995	ENU10790	ANI61C1795: 651..301			GSP								
26996	ENU10791	ANI61C1059 9:1166..697			GSP								
26997	ENU10792	ANI61C1005: 159..644			GSP								
26998	ENU10793	ANI61C8215: 808..223			GSP								
26999	ENU10794	ANI61C8218: 800..126			GSP								
27000	ENU10795	ANI61C655:6 67..230			GSP								
27001	ENU10796	ANI61C7509: 665..59			GSP								

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr%	Description
27016	ENU10811	ANI61C6825:1110..1553			GSP								
27017	ENU10812	ANI61C6826:892..1134			GSP								
27018	ENU10813	ANI61C8285:680..1088			GSP								
27019	ENU10814	ANI61C11188:1202..234			GSP								
27020	ENU10815	ANI61C6833:47..594			GSP								
27021	ENU10816	ANI61C6845:1225..1545			GSP								
27022	ENU10817	ANI61C6869:444..49			GSP								
27023	ENU10818	ANI61C6876:1362..467			GSP								
27024	ENU10819	ANI61S544:296..29			GSP								
27025	ENU10820	ANI61C3201:1463..2118			GSP								
27026	ENU10821	ANI61C3206:906..20			GSP								
27027	ENU10822	ANI61C3220:676..904			GSP								

Gene annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
27028	ENU10823	ANI61C3223:111..491			GSP								
27029	ENU10824	ANI61S582:342..4			GSP								
27030	ENU10825	ANI61S1603:33..296			GSP								
27031	ENU10826	ANI61C2502:1047..297			GSP								
27032	ENU10827	ANI61S3077:561..69			GSP								
27033	ENU10828	ANI61C11316:726..373			GSP								
27034	ENU10829	ANI61S2355:2..446			GSP								
27035	ENU10830	ANI61C11323:1295..421			GSP								
27036	ENU10831	ANI61C11334:127..375			GSP								
27037	ENU10832	ANI61S2374:80..323			GSP								
27038	ENU10833	ANI61C2548:2501..2814			GSP								
27039	ENU10834	ANI61C10612:640..35			GSP								
27040	ENU10835	ANI61S2386:120..347			GSP								
27041	ENU10836	ANI61C1820:1305..1067			GSP								

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr%	Description
27042	ENU10837	ANI61C2551:593..144			GSP								
27043	ENU10838	ANI61C1825:96..480			GSP								
27044	ENU10839	ANI61C1827:63..511			GSP								
27045	ENU10840	ANI61C2557:358..11			GSP								
27046	ENU10841	ANI61S1665:225..14			GSP								
27047	ENU10842	ANI61C2564:1021..556			GSP								
27048	ENU10843	ANI61C2564:3000..3693			GSP								
27049	ENU10844	ANI61C2565:1843..1553			GSP								
27050	ENU10845	ANI61C11360:423..744			GSP								
27051	ENU10846	ANI61C11361:314..753			GSP								
27052	ENU10847	ANI61C11365:615..94			GSP								
27053	ENU10848	ANI61C11370:1053..437			GSP								

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	Description
27081	ENU10876	ANI61C6912:1483..1817			GSP								
27082	ENU10877	ANI61C7644:445..945			GSP								
27083	ENU10878	ANI61C8385:774..119			GSP								
27084	ENU10879	ANI61C6940:1685..2623			GSP								
27085	ENU10880	ANI61S606:33..278			GSP								
27086	ENU10881	ANI61C7683:56..815			GSP								
27087	ENU10882	ANI61C7685:651..899			GSP								
27088	ENU10883	ANI61C6973:58..857			GSP								
27089	ENU10884	ANI61C4000:2436..2718			GSP								
27090	ENU10885	ANI61C38:2780..4266			GSP								
27091	ENU10886	ANI61C6988:654..79			GSP								
27092	ENU10887	ANI61C4014:1281..1520			GSP								
27093	ENU10888	ANI61C47:516..59			GSP								
27094	ENU10889	ANI61C4030:795..365			GSP								

Gene annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
27095	ENU10890	ANI61C4033: 64..360			GSP								
27096	ENU10891	ANI61S3149: 137..451			GSP								
27097	ENU10892	ANI61C4041: 33..770			GSP								
27098	ENU10893	ANI61C3319: 449..210			GSP								
27099	ENU10894	ANI61C87:13 60..758			GSP								
27100	ENU10895	ANI61C90:28 ..383			GSP								
27101	ENU10896	ANI61C9734: 25-46 136..1020	25-46	755-777	GSP								
27102	ENU10897	ANI61C4069: 483..163			GSP								
27103	ENU10898	ANI61C1140 4:3057..1670			GSP								
27104	ENU10899	ANI61C1140 5:362..983			GSP								
27105	ENU10900	ANI61C1140 8:48..1109			GSP								
27106	ENU10901	ANI61C4075: 1168..899			GSP								
27107	ENU10902	ANI61S1726: 161..580			GSP								
27108	ENU10903	ANI61C2623: 769..1152			GSP								
27109	ENU10904	ANI61C3354: 1852..823			GSP								

GenBank accession

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr g	Description
27110	ENU10905	ANI61C4083:600..292			GSP								
27111	ENU10906	ANI61C2631:569..96			GSP								
27112	ENU10907	ANI61C2634:575..63			GSP								
27113	ENU10908	ANI61C4098:3119..2841			GSP								
27114	ENU10909	ANI61C11437:2736..3185			GSP								
27115	ENU10910	ANI61C1911:743..462			GSP								
27116	ENU10911	ANI61C1917:658..913			GSP								
27117	ENU10912	ANI61C3375:274..515			GSP								
27118	ENU10913	ANI61C726:125-43519..2739	1184-1203		GSP								
27119	ENU10914	ANI61C3384:522..319			GSP								
27120	ENU10915	ANI61C11453:1122..904			GSP								
27121	ENU10916	ANI61C10726:39..550			GSP								
27122	ENU10917	ANI61S1762:138..449			GSP								
27123	ENU10918	ANI61C10728:504..109			GSP								
27124	ENU10919	ANI61C11458:498..226			GSP								

Gene annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr%	Description
27125	ENU10920	ANI61C1936:1249..1759			GSP								
27126	ENU10921	ANI61C3394:507..1723			GSP								
27127	ENU10922	ANI61C3396:134..527			GSP								
27128	ENU10923	ANI61C1939:555..292			GSP								
27129	ENU10924	ANI61C11463:2680..3042			GSP								
27130	ENU10925	ANI61S1771:153..362			GSP								
27131	ENU10926	ANI61C2671:319..23			GSP								
27132	ENU10927	ANI61C2672:34..605			GSP								
27133	ENU10928	ANI61C10746:1645..1439			GSP								
27134	ENU10929	ANI61C1950:26..509			GSP								
27135	ENU10930	ANI61C1955:841..1119			GSP								
27136	ENU10931	ANI61C10773:3044..2808			GSP								
27137	ENU10932	ANI61C1987:421..25			GSP								
27138	ENU10933	ANI61C9739:25-451081..2142		1020-1044	GSP								
27139	ENU10934	ANI61C815:505..807			GSP								

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
27140	ENU10935	ANI61C9119:670..385			GSP								
27141	ENU10936	ANI61C1993:578..104			GSP								
27142	ENU10937	ANI61C10797:3932..3549			GSP								
27143	ENU10938	ANI61C9132:954..398			GSP								
27144	ENU10939	ANI61C840:49..456			GSP								
27145	ENU10940	ANI61C849:1187..1681			GSP								
27146	ENU10941	ANI61C876:1590..2086			GSP								
27147	ENU10942	ANI61C7712:42..2293			GSP								
27148	ENU10943	ANI61C9179:6801..6508			GSP								
27149	ENU10944	ANI61C881:819..1067			GSP								
27150	ENU10945	ANI61C7726:1811..2377			GSP								
27151	ENU10946	ANI61C9186:546..1025			GSP								
27152	ENU10947	ANI61C7728:17..352			GSP								
27153	ENU10948	ANI61C8461:1237..130			GSP								

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
27154	ENU10949	ANI61C7733:545..1042			GSP								
27155	ENU10950	ANI61C8464:2369..2686			GSP								
27156	ENU10951	ANI61C9194:509..45			GSP								
27157	ENU10952	ANI61C7738:773..1078			GSP								
27158	ENU10953	ANI61C8477:600..325			GSP								
27159	ENU10954	ANI61C7750:935..549			GSP								
27160	ENU10955	ANI61C8483:2739..1493			GSP								
27161	ENU10956	ANI61C7758:582..1060			GSP								
27162	ENU10957	ANI61C8488:2420..2040			GSP								
27163	ENU10958	ANI61S10:388..158			GSP								
27164	ENU10959	ANI61C7772:1779..2054			GSP								
27165	ENU10960	ANI61S704:290..69			GSP								
27166	ENU10961	ANI61C7784:33..440			GSP								
27167	ENU10962	ANI61S3210:133..504			GSP								

Gene description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
27168	ENU10963	ANI61S54:41 6..84			GSP								
27169	ENU10964	ANI61S57:40 5..27			GSP								
27170	ENU10965	ANI61C4111: 381..989			GSP								
27171	ENU10966	ANI61C4118: 1219..627			GSP								
27172	ENU10967	ANI61S62:39 2..105			GSP								
27173	ENU10968	ANI61C4136: 1820..2838			GSP								
27174	ENU10969	ANI61S80:90. .302			GSP								
27175	ENU10970	ANI61C8145: 25-48 425..2575	1462- 1497		GSP								
27176	ENU10971	ANI61S786:8 57..26			GSP								
27177	ENU10972	ANI61C2704: 1830..1507			GSP								
27178	ENU10973	ANI61C4171: 1698..76			GSP								
27179	ENU10974	ANI61C3448: 29..325			GSP								
27180	ENU10975	ANI61C3467: 382..22			GSP								
27181	ENU10976	ANI61C3469: 29..429			GSP								
27182	ENU10977	ANI61C2740: 1333..855			GSP								

Genomic Coordinates

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr g	Description
27183	ENU10978	ANI61C2762: 566..303			GSP								
27184	ENU10979	ANI61C6697: 25-46 2040..2513	428-456		GSP								
27185	ENU10980	ANI61S1889: 276..489			GSP								
27186	ENU10981	ANI61C1085 3:912..3556			GSP								
27187	ENU10982	ANI61C1085 7:388..684			GSP								
27188	ENU10983	ANI61C2796: 651..1025			GSP								
27189	ENU10984	ANI61C910:2 343..2119			GSP								
27190	ENU10985	ANI61C1088 3:1002..601			GSP								
27191	ENU10986	ANI61C9218: 232..642			GSP								
27192	ENU10987	ANI61C927:2 538..2790			GSP								
27193	ENU10988	ANI61C9232: 396..1202			GSP								
27194	ENU10989	ANI61C944:1 483..1128			GSP								
27195	ENU10990	ANI61C8518: 97..1204			GSP								
27196	ENU10991	ANI61C950:3 56..47			GSP								
27197	ENU10992	ANI61C8529: 4191..4479			GSP								

Gene Description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
27198	ENU10993	ANI61C963:1 068..1394			GSP								
27199	ENU10994	ANI61C9261: 723..1335			GSP								
27200	ENU10995	ANI61C8533: 199..436			GSP								
27201	ENU10996	ANI61C8534: 3831..4522			GSP								
27202	ENU10997	ANI61C8539: 1603..2387			GSP								
27203	ENU10998	ANI61C8543: 3298..2891			GSP								
27204	ENU10999	ANI61C7818: 15..251			GSP								
27205	ENU11000	ANI61C9283: 759..70			GSP								
27206	ENU11001	ANI61C9284: 569..336			GSP								
27207	ENU11002	ANI61C9284: 2239..1572			GSP								
27208	ENU11003	ANI61C7852: 17..259			GSP								
27209	ENU11004	ANI61C7868: 1327..541			GSP								
27210	ENU11005	ANI61C7532: 25-48 5139..3735		1200- 1227	GSP								
27211	ENU11006	ANI61C7889: 134..827			GSP								
27212	ENU11007	ANI61C4201: 651..966			GSP								

Gene annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
27213	ENU11008	ANI61C4231:1045..2050			GSP								
27214	ENU11009	ANI61C4240:1802..1443			GSP								
27215	ENU11010	ANI61S870:75..413			GSP								
27216	ENU11011	ANI61S887:533..71			GSP								
27217	ENU11012	ANI61S1900:242..36			GSP								
27218	ENU11013	ANI61S3362:59..322			GSP								
27219	ENU11014	ANI61C4253:25-50390..2994	2512-2538		GSP								
27220	ENU11015	ANI61C2823:703..311			GSP								
27221	ENU11016	ANI61S1936:3..307			GSP								
27222	ENU11017	ANI61C3564:2741..2421			GSP								
27223	ENU11018	ANI61C4294:945..11			GSP								
27224	ENU11019	ANI61C10903:2408..2130			GSP								
27225	ENU11020	ANI61C10909:1207..1480			GSP								
27226	ENU11021	ANI61C3574:621..271			GSP								
27227	ENU11022	ANI61C2851:338..80			GSP								

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
27257	ENU11052	ANI61C3604:172..483			GSP								
27258	ENU11053	ANI61C5067:528..11			GSP								
27259	ENU11054	ANI61C4339:641..103			GSP								
27260	ENU11055	ANI61S3440:247..33			GSP								
27261	ENU11056	ANI61C4340:1106..646			GSP								
27262	ENU11057	ANI61C8097:25-52180..794	572-597		GSP								
27263	ENU11058	ANI61C3625:410..209			GSP								
27264	ENU11059	ANI61C4355:23..1006			GSP								
27265	ENU11060	ANI61S986:244..16			GSP								
27266	ENU11061	ANI61S987:230..502			GSP								
27267	ENU11062	ANI61C2904:49..527			GSP								
27268	ENU11063	ANI61C5091:394..26			GSP								
27269	ENU11064	ANI61C5092:565..249			GSP								
27270	ENU11065	ANI61C5099:1694..1380			GSP								
27271	ENU11066	ANI61S3475:342..2			GSP								

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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
27316	ENU11111	ANI61C3754: 3331..3726			GSP								
27317	ENU11112	ANI61C3761: 33..389			GSP								
27318	ENU11113	ANI61C3784: 637..260			GSP								
27319	ENU11114	ANI61C3784: 972..1225			GSP								
27320	ENU11115	ANI61C3791: 28..648			GSP								
27321	ENU11116	ANI61C9503: 1086..832			GSP								
27322	ENU11117	ANI61C8804: 20..376			GSP								
27323	ENU11118	ANI61C9553: 5754..6136			GSP								
27324	ENU11119	ANI61C8826: 1028..2376			GSP								
27325	ENU11120	ANI61C9579: 588..247			GSP								
27326	ENU11121	ANI61C8850: 1149..554			GSP								
27327	ENU11122	ANI61C9580: 3119..2889			GSP								
27328	ENU11123	ANI61C8890: 3006..2620			GSP								
27329	ENU11124	ANI61C8891: 1547..1314			GSP								

Gene Ontology

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
27359	ENU111154	ANI61C6037: 45..452			GSP								
27360	ENU111155	ANI61C6049: 2643..2927			GSP								
27361	ENU111156	ANI61C6054: 617..180			GSP								
27362	ENU111157	ANI61C5326: 269..673			GSP								
27363	ENU111158	ANI61C6063: 548..247			GSP								
27364	ENU111159	ANI61C4630: 121..563			GSP								
27365	ENU111160	ANI61C5365: 985..1310			GSP								
27366	ENU111161	ANI61S4484: 249..611			GSP								
27367	ENU111162	ANI61C3921: 953..1335			GSP								
27368	ENU111163	ANI61C3921: 2779..2390			GSP								
27369	ENU111164	ANI61C4653: 2087..1719			GSP								
27370	ENU111165	ANI61C4654: 1614..1315			GSP								
27371	ENU111166	ANI61C4658: 914..174			GSP								
27372	ENU111167	ANI61S3763: 74..559			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
27416	ENU11211	ANI61C1192: 974..1474			GSP								
27417	ENU11212	ANI61C9847: 6199..6726			GSP								
27418	ENU11213	ANI61C9867: 1066..34			GSP								
27419	ENU11214	ANI61C9891: 452..243			GSP								
27420	ENU11215	ANI61C9899: 47..334			GSP								
27421	ENU11216	ANI61C6223: 92..463			GSP								
27422	ENU11217	ANI61S4621: 277..516			GSP								
27423	ENU11218	ANI61C5522: 613..402			GSP								
27424	ENU11219	ANI61C6258: 4017..4280			GSP								
27425	ENU11220	ANI61C4802: 291..4			GSP								
27426	ENU11221	ANI61C5533: 1131..1565			GSP								
27427	ENU11222	ANI61C5535: 1669..2031			GSP								
27428	ENU11223	ANI61C6268: 1609..1048			GSP								
27429	ENU11224	ANI61C4818: 1055..79			GSP								

Table 6.6.6

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
27430	ENU11225	ANI61C6280: 695..384			GSP								
27431	ENU11226	ANI61C1085 25-42		1030-1050	GSP								
27432	ENU11227	ANI61C6289: 635..118			GSP								
27433	ENU11228	ANI61C5562: 115..501			GSP								
27434	ENU11229	ANI61C4861: 232..549			GSP								
27435	ENU11230	ANI61C4883: 540..944			GSP								
27436	ENU11231	ANI61C4886: 692..387			GSP								
27437	ENU11232	ANI61C4888: 735..28			GSP								
27438	ENU11233	ANI61C1000 5:1..846			GSP								
27439	ENU11234	ANI61C1212: 2420..1437			GSP								
27440	ENU11235	ANI61C1212: 7293..7081			GSP								
27441	ENU11236	ANI61C1215: 1067..828			GSP								
27442	ENU11237	ANI61C1001 9:66..374			GSP								
27443	ENU11238	ANI61C1001 9:1431..1786			GSP								
27444	ENU11239	ANI61S1058: 463..56			GSP								

GenBank

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
27445	ENU11240	ANI61C1002 4:388..146			GSP								
27446	ENU11241	ANI61C1004 2:147..493			GSP								
27447	ENU11242	ANI61C3535: 25-47 237..1526	1027-	1050	GSP								
27448	ENU11243	ANI61C5361: 25-49 1482..2129	606-630		GSP								
27449	ENU11244	ANI61C1043 25-43 6:4516..4046	434-453		GSP								
27450	ENU11245	ANI61C8290: 25-50 534..196	296-321		GSP								
27451	ENU11246	ANI61C8406: 25-48 1268..512	723-747		GSP								
27452	ENU11247	ANI61C3560: 25-50 547..1	736-762		GSP								
27453	ENU11248	ANI61C9221: 25-48 3343..4865	1159-	1182	GSP								
27454	ENU11249	ANI61C9335: 25-53 79..726	605-630		GSP								
27455	ENU11250	ANI61C4319: 25-48 596..2490	1770-	1794	GSP								
27456	ENU11251	ANI61C1135 25-54 4:738..97	598-624		GSP								
27457	ENU11252	ANI61C9630: 25-54 6026..5230	693-723		GSP								
27458	ENU11253	ANI61C3:451 25-49 ..1	487-516		GSP								
27459	ENU11254	ANI61C3101: 25-56 38..1916	1124-	1152	GSP								
27460	ENU11255	ANI61C7406: 25-51 933..374	473-492		GSP								
27461	ENU11256	ANI61C2199: 25-42 808..1	822-843		GSP								
27462	ENU11257	ANI61C1140 25-44 4:2738..1670	829-855		GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
27482	ENU11277	ANI61C1044 6:7194..6514	25-51	639-663	GSP								
27483	ENU11278	ANI61C8003: 25-52 1818..1891	25-52	1057-1086	GSP								
27484	ENU11279	ANI61C8107: 25-43 713..2196	25-43	1246-1269	GSP								
27485	ENU11280	ANI61C7096: 25-42 132..1272	25-42	1035-1062	GSP								
27486	ENU11281	ANI61C1232: 25-45 2724..1345	25-45	1117-1146	GSP								
27487	ENU11282	ANI61C1097 25-49 9:137..967	25-49	733-750	GSP								
27488	ENU11283	ANI61C5397: 25-43 1095..2412	25-43	1232-1254	GSP								
27489	ENU11284	ANI61C3282: 25-48 159..1181	25-48	979-1005	GSP								
27490	ENU11285	ANI61C9348: 25-53 3299..2421	25-53	797-819	GSP								
27491	ENU11286	ANI61C4800: 25-43 1832..3077	25-43	1279-1311	GSP								
27492	ENU11287	ANI61C4256: 25-51 566..33	25-51	493-516	GSP								
27493	ENU11288	ANI61C1134 25-50 6:1472..487	25-50	810-834	GSP								
27494	ENU11289	ANI61C4213: 25-47 1527..671	25-47	758-780	GSP								
27495	ENU11290	ANI61C479:3 25-49 3..473	25-49	395-423	GSP								
27496	ENU11291	ANI61C6489: 25-48 268..3596	25-48	2459-2490	GSP								
27497	ENU11292	ANI61C2618: 25-51 90..965	25-51	836-858	GSP								
27498	ENU11293	ANI61C5742: 25-43 957..452	25-43	473-495	GSP								
27499	ENU11294	ANI61C1141 25-56 9:151..1266	25-56	1066-1098	GSP								
27500	ENU11295	ANI61C35:19 25-45 89..684	25-45	1075-1092	GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
27501	ENU11296	ANI61C9640: 25-48 121..569	25-48	412-438	GSP								
27502	ENU11297	ANI61C6944: 25-50 2214..514	25-50	1601-1632	GSP								
27503	ENU11298	ANI61C1072: 25-51 2588..3558	25-51	862-891	GSP								
27504	ENU11299	ANI61C1075 25-53 2:1..831	25-53	1134-1167	GSP								
27505	ENU11300	ANI61C1651: 25-51 2327..2689	25-51	324-345	GSP								
27506	ENU11301	ANI61C4544: 25-47 485..1764	25-47	872-897	GSP								
27507	ENU11302	ANI61C9753: 25-55 495..1130	25-55	589-618	GSP								
27508	ENU11303	ANI61C1040 25-48 4:3494..3038	25-48	438-459	GSP								
27509	ENU11304	ANI61C3663: 25-50 53..781	25-50	685-711	GSP								
27510	ENU11305	ANI61C8074: 25-52 1760..2561	25-52	625-654	GSP								
27511	ENU11306	ANI61C8623: 25-48 4801..5229	25-48	405-435	GSP								
27512	ENU11307	ANI61C9552: 25-46 2908..1237	25-46	1428-1458	GSP								
27513	ENU11308	ANI61C6472: 25-48 135..851	25-48	674-699	GSP								
27514	ENU11309	ANI61C1041 25-45 7:735..1262	25-45	487-510	GSP								
27515	ENU11310	ANI61C1006: 25-45 2144..2787	25-45	609-630	GSP								
27516	ENU11311	ANI61C8909: 25-54 2220..2828	25-54	571-594	GSP								
27517	ENU11312	ANI61C895:3 25-50 078..1361	25-50	1010-1035	GSP								
27518	ENU11313	ANI61C7397: 25-48 7..963	25-48	906-939	GSP								
27519	ENU11314	ANI61C5665: 25-48 1634..2017	25-48	341-366	GSP								

GenBank Submission

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
27520	ENU11315	ANI61C8180: 25-51 381..894	25-51	517-543	GSP								
27521	ENU11316	ANI61C1008 25-51 9:1402..454	25-51	907-930	GSP								
27522	ENU11317	ANI61C7548: 25-48 252..899	25-48	597-630	GSP								
27523	ENU11318	ANI61C9033: 25-52 2175..2843	25-52	1093-1116	GSP								
27524	ENU11319	ANI61C5893: 25-54 133..714	25-54	543-567	GSP								
27525	ENU11320	ANI61C2666: 25-46 4964..4109	25-46	755-780	GSP								
27526	ENU11321	ANI61C9776: 25-50 4636..2066	25-50	2275-2298	GSP								
27527	ENU11322	ANI61C9714: 25-48 1172..687	25-48	445-468	GSP								
27528	ENU11323	ANI61C1103 25-46 8:1841..956	25-46	808-828	GSP								
27529	ENU11324	ANI61C9251: 25-51 4545..3844	25-51	660-684	GSP								
27530	ENU11325	ANI61C6165: 25-42 297..605	25-42	267-291	GSP								
27531	ENU11326	ANI61C1252: 25-48 2607..4768	25-48	1486-1509	GSP								
27532	ENU11327	ANI61C7675: 25-48 2330..4510	25-48	1935-1959	GSP								
27533	ENU11328	ANI61C1022 25-44 7:997..1659	25-44	627-645	GSP								
27534	ENU11329	ANI61C1026 25-55 0:857..2059	25-55	906-930	GSP								
27535	ENU11330	ANI61C1019 25-46 8:23..1003	25-46	858-885	GSP								
27536	ENU11331	ANI61C7931: 25-48 674..357	25-48	276-300	GSP								
27537	ENU11332	ANI61C7943: 25-45 3406..2876	25-45	488-513	GSP								
27538	ENU11333	ANI61C8830: 25-47 3094..1628	25-47	1289-1314	GSP								

GeneSet

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
27558	ENU11353	ANI61C8197: 866..1405	25-54	497-522	GSP								
27559	ENU11354	ANI61C8501: 1199..732	25-46	424-450	GSP								
27560	ENU11355	ANI61C7392: 1307..612	25-48	655-678	GSP								
27561	ENU11356	ANI61C7053: 1220..629	25-60	541-573	GSP								
27562	ENU11357	ANI61C1804: 1787..773	25-47	755-774	GSP								
27563	ENU11358	ANI61C1355: 1254..2042	25-52	584-609	GSP								
27564	ENU11359	ANI61C2838: 6425..6087	25-45	295-321	GSP								
27565	ENU11360	ANI61C1086 4:3344..3613	25-47	229-255	GSP								
27566	ENU11361	ANI61C1146 1:2212..1167	25-58	1005-1029	GSP								
27567	ENU11362	ANI61C4813: 4104..4746	25-45	531-555	GSP								
27568	ENU11363	ANI61C1814: 2039..1032	25-52	911-939	GSP								
27569	ENU11364	ANI61C7559: 4250..3190	25-47	1058-1086	GSP								
27570	ENU11365	ANI61C9673: 3334..4958	25-48	963-990	GSP								
27571	ENU11366	ANI61C4359: 3326..1254	25-49	1760-1791	GSP								
27572	ENU11367	ANI61C260:7 1..464	25-46	381-405	GSP								
27573	ENU11368	ANI61C136:2 563..3117	25-47	542-567	GSP								
27574	ENU11369	ANI61C5892: 2984..2430	25-49	511-537	GSP								
27575	ENU11370	ANI61C322:1 3897..12947	25-48	907-933	GSP								
27576	ENU11371	ANI61C96:26 58..2218	25-53	396-423	GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
27577	ENU11372	ANI61C7532: 1878..2936	25-48	956-990	GSP								
27578	ENU11373	ANI61C3691: 1666..1058	25-57	567-591	GSP								
27579	ENU11374	ANI61C6754: 2578..2977	25-47	354-387	GSP								
27580	ENU11375	ANI61C1695: 2048..1590	25-53	412-441	GSP								
27581	ENU11376	ANI61C9665: 1466..933	25-44	499-516	GSP								
27582	ENU11377	ANI61C5460: 418..86	25-53	289-315	GSP								
27583	ENU11378	ANI61C8016: 4563..5658	25-47	1001-1026	GSP								
27584	ENU11379	ANI61C1032: 6:526..126	25-52	368-390	GSP								
27585	ENU11380	ANI50C1_16: 62:883..2658	25-51	2072-2097	GSP								
27586	ENU11381	ANI61C1043: 3:6045..5383	25-46	636-657	GSP								
27587	ENU11382	ANI61C1800: 2853..4234	25-44	1264-1281	GSP								
27588	ENU11383	ANI61C1118: 5:6336..4674	25-48	1323-1350	GSP								
27589	ENU11384	ANI61C7218: 2298..1016	25-46	1191-1212	GSP								
27590	ENU11385	ANI61C1135: 0:1359..814	25-45	502-528	GSP								
27591	ENU11386	ANI61C7821: 120..1235	25-43	1004-1029	GSP								
27592	ENU11387	ANI61C1030: 0:6596..8562	25-47	1600-1626	GSP								
27593	ENU11388	ANI61C7114: 919..1173	25-48	210-240	GSP								
27594	ENU11389	ANI61C8869: 652..1	25-54	1118-1143	GSP								
27595	ENU11390	ANI61C9317: 1013..2138	25-60	1033-1056	GSP								

Gene description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
27596	ENU11391	ANI61C3861: 1592..4032	25-47	959-981	GSP								
27597	ENU11392	ANI61C1756: 871..1219	25-49	308-333	GSP								
27598	ENU11393	ANI61C5231: 1674..696	25-44	894-918	GSP								
27599	ENU11394	ANI61C9788: 2539..3917	25-47	1185-1203	GSP								
27600	ENU11395	ANI61C9195: 1475..1239	25-47	194-219	GSP								
27601	ENU11396	ANI61C6617: 3155..4344	25-52	1122-1152	GSP								
27602	ENU11397	ANI61C6535: 1511..1177	25-49	296-318	GSP								
27603	ENU11398	ANI61C9071: 1813..3126	25-46	1206-1230	GSP								
27604	ENU11399	ANI61C1739: 1900..2871	25-42	850-873	GSP								
27605	ENU11400	ANI50S1653: 430..35	25-49	349-378	GSP								
27606	ENU11401	ANI61C3457: 487..1486	25-50	962-987	GSP								
27607	ENU11402	ANI61C1475: 138..605	25-48	425-450	GSP								
27608	ENU11403	ANI61C2359: 482..865	25-53	341-366	GSP								
27609	ENU11404	ANI61C3844: 1874..2723	25-43	686-714	GSP								
27610	ENU11405	ANI61C5924: 5506..6654	25-45	1108-1131	GSP								
27611	ENU11406	ANI61C5371: 689..107	25-43	329-348	GSP								
27612	ENU11407	ANI61C2188: 18..500	25-44	443-465	GSP								
27613	ENU11408	ANI61C5986: 769..1257	25-46	448-471	GSP								
27614	ENU11409	ANI61C876:3 855..2439	25-54	1203-1224	GSP								

1. The first part of the document is a list of references. The references are listed in a standard format, with the author's name, the title of the work, and the publisher. The references are as follows:

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
27615	ENU11410	ANI61C933:1 18..759	25-46	600-624	GSP								
27616	ENU11411	ANI61C8913:1029..1775	25-54	550-579	GSP								
27617	ENU11412	ANI61C7276:4864..4605	25-57	221-252	GSP								
27618	ENU11413	ANI61C2256:1735..606	25-47	1025-1047	GSP								
27619	ENU11414	ANI61C1054:4:503..953	25-50	407-435	GSP								
27620	ENU11415	ANI61C9758:1291..272	25-50	972-1002	GSP								
27621	ENU11416	ANI61C5574:2590..856	25-48	1435-1467	GSP								
27622	ENU11417	ANI61C4363:1260..137	25-42	1043-1062	GSP								
27623	ENU11418	ANI61C1099:7:2080..108	25-49	1061-1086	GSP								
27624	ENU11419	ANI50C1_17:81:936..1	25-49	996-1023	GSP								
27625	ENU11420	ANI61C7914:563..1938	25-49	1131-1155	GSP								
27626	ENU11421	ANI61C3038:213..730	25-47	476-501	GSP								
27627	ENU11422	ANI61C7020:2298..3054	25-45	657-684	GSP								
27628	ENU11423	ANI61C1059:1:1229..1702	25-47	494-522	GSP								
27629	ENU11424	ANI61C192:7:3..90	25-48	993-1020	GSP								
27630	ENU11425	ANI61C568:4:528..5616	25-57	1010-1038	GSP								
27631	ENU11426	ANI61C9927:853..1380	25-51	481-510	GSP								
27632	ENU11427	ANI61C7519:2104..4116	25-48	1284-1308	GSP								
27633	ENU11428	ANI61C4745:2939..1121	25-43	534-558	GSP								

Table 3: Gene annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
27653	ENU11448	ANI61C1307: 25-47 162..777	25-47	498-525	GSP								
27654	ENU11449	ANI61C6595: 25-53 407..83	25-53	283-306	GSP								
27655	ENU11450	ANI61C563:4 25-56 233..3763	25-56	418-453	GSP								
27656	ENU11451	ANI61C1467: 25-60 2609..701	25-60	1564-1587	GSP								
27657	ENU11452	ANI61C9661: 25-42 943..2650	25-42	1463-1491	GSP								
27658	ENU11453	ANI61C1899: 25-49 279..1569	25-49	1051-1077	GSP								
27659	ENU11454	ANI61C314:3 25-45 569..3009	25-45	523-543	GSP								
27660	ENU11455	ANI61C4652: 25-45 4539..3879	25-45	623-642	GSP								
27661	ENU11456	ANI61C7344: 25-46 553..1427	25-46	717-744	GSP								
27662	ENU11457	ANI61C1102: 25-49 1007..399	25-49	533-552	GSP								
27663	ENU11458	ANI61C1103 25-48 0:990..2243	25-48	1184-1206	GSP								
27664	ENU11459	ANI61C5963: 25-48 1484..775	25-48	683-711	GSP								
27665	ENU11460	ANI61C2577: 25-45 1..920	25-45	853-876	GSP								
27666	ENU11461	ANI61C7847: 25-55 934..2031	25-55	943-966	GSP								
27667	ENU11462	ANI61C1359: 25-47 1154..759	25-47	355-378	GSP								
27668	ENU11463	ANI61C4272: 25-52 1785..2238	25-52	406-435	GSP								
27669	ENU11464	ANI61C3320: 25-49 3935..2344	25-49	1488-1518	GSP								
27670	ENU11465	ANI61C3350: 25-46 544..3	25-46	508-528	GSP								
27671	ENU11466	ANI61C9980: 25-48 1297..2692	25-48	1290-1317	GSP								

Gene Description

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
27672	ENU11467	ANI61C882:5 6..977	25-44	758-783	GSP								
27673	ENU11468	ANI61C9307: 2057..1566	25-42	441-465	GSP								
27674	ENU11469	ANI61C1124 9:1741..316	25-58	1238-1266	GSP								
27675	ENU11470	ANI61C1001 3:112..515	25-48	363-390	GSP								
27676	ENU11471	ANI61C8854: 2501..3411	25-48	854-879	GSP								
27677	ENU11472	ANI61C4876: 2800..1012	25-47	1644-1674	GSP								
27678	ENU11473	ANI61C7173: 5929..5225	25-50	533-564	GSP								
27679	ENU11474	ANI61C8248: 2447..1223	25-46	1181-1206	GSP								
27680	ENU11475	ANI61C2533: 2792..1137	25-51	574-606	GSP								
27681	ENU11476	ANI61C6294: 3387..2965	25-42	326-348	GSP								
27682	ENU11477	ANI61C464:1 543..3274	25-46	1075-1107	GSP								
27683	ENU11478	ANI61C9211: 841..463	25-43	342-363	GSP								
27684	ENU11479	ANI61C6804: 8679..9269	25-47	550-573	GSP								
27685	ENU11480	ANI61C2881: 505..23	25-48	432-465	GSP								
27686	ENU11481	ANI61C8985: 1757..702	25-42	854-882	GSP								
27687	ENU11482	ANI61C5083: 691..329	25-47	327-345	GSP								
27688	ENU11483	ANI61C1139 7:3768..2577	25-48	1118-1143	GSP								
27689	ENU11484	ANI61C6772: 2789..4449	25-51	904-936	GSP								
27690	ENU11485	ANI61C9746: 1356..2228	25-51	748-771	GSP								

Gene annotation

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
27691	ENU11486	ANI61C4946: 609..1052	25-44	403-426	GSP								
27692	ENU11487	ANI61C7341: 541..603	25-45	729-756	GSP								
27693	ENU11488	ANI61C6284: 7676..7242	25-53	515-540	GSP								
27694	ENU11489	ANI61C1040 1:3381..2461	25-52	879-903	GSP								
27695	ENU11490	ANI61C9107: 478..1571	25-53	748-774	GSP								
27696	ENU11491	ANI61C9874: 774..512	25-48	225-255	GSP								
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27699	ENU11494	ANI61C3155: 481..94	25-53	343-369	GSP								
27700	ENU11495	ANI61C8709: 61..986	25-42	834-855	GSP								
27701	ENU11496	ANI61C1107 3:5723..4794	25-47	755-777	GSP								
27702	ENU11497	ANI61C914:2 931..3284	25-52	307-336	GSP								
27703	ENU11498	ANI61C4106: 533..1172	25-55	475-498	GSP								
27704	ENU11499	ANI61C7970: 2763..3219	25-51	416-438	GSP								
27705	ENU11500	ANI50S6383: 13..372	25-54	321-342	GSP								
27706	ENU11501	ANI61C6472: 1637..1182	25-54	411-438	GSP								
27707	ENU11502	ANI61C8244: 480..770	25-46	249-273	GSP								
27708	ENU11503	ANI61C1019 7:5179..4682	25-48	410-438	GSP								
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GenBank Submission

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27712	ENU11507	ANI61C2688: 3750..5147	25-48	1090-1116	GSP								
27713	ENU11508	ANI61S105:2 47..513	25-45	227-249	GSP								
27714	ENU11509	ANI61C4242: 1336..1031	25-49	261-288	GSP								
27715	ENU11510	ANI61C6934: 803..97	25-60	2030-2055	GSP								
27716	ENU11511	ANI61S829:4 54..167	25-54	238-270	GSP								
27717	ENU11512	ANI61C2036: 438..109	25-51	292-315	GSP								
27718	ENU11513	ANI61C2577: 1478..1074	25-53	499-519	GSP								
27719	ENU11514	ANI61C3701: 4036..4338	25-52	250-285	GSP								
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27721	ENU11516	ANI61C7269: 2616..1530	25-48	907-933	GSP								
27722	ENU11517	ANI61C8731: 4102..1416	25-43	1465-1494	GSP								
27723	ENU11518	ANI61C7573: 436..885	25-44	405-432	GSP								
27724	ENU11519	ANI61C9156: 597..73	25-43	485-507	GSP								
27725	ENU11520	ANI61C3399: 2610..1263	25-49	1236-1263	GSP								
27726	ENU11521	ANI61C7310: 4839..4856	25-53	1031-1056	GSP								
27727	ENU11522	ANI61C2940: 436..59	25-48	325-360	GSP								
27728	ENU11523	ANI61C3578: 1486..2709	25-56	729-759	GSP								

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27731	ENU11526	ANI61C9171: 25-48 1959..597	25-48	1111- 1146	GSP								
27732	ENU11527	ANI61C59:18 25-43 74..3318	25-43	1276- 1296	GSP								
27733	ENU11528	ANI61C7697: 25-51 2063..382	25-51	1409- 1440	GSP								
27734	ENU11529	ANI61C3180: 25-48 248..1172	25-48	633-660	GSP								
27735	ENU11530	ANI61C1148 25-45 4:737..1733	25-45	821-846	GSP								
27736	ENU11531	ANI61C3701: 25-48 3089..3358	25-48	228-252	GSP								
27737	ENU11532	ANI61C1060 25-42 3:2742..1457	25-42	1103- 1128	GSP								
27738	ENU11533	ANI61C5772: 25-51 406..35	25-51	334-354	GSP								
27739	ENU11534	ANI61C2468: 25-45 2924..3410	25-45	492-522	GSP								
27740	ENU11535	ANI61C7430: 25-46 3283..2845	25-46	704-735	GSP								
27741	ENU11536	ANI61C634:3 25-49 6..485	25-49	406-432	GSP								
27742	ENU11537	ANI61C3266: 25-54 674..1356	25-54	579-603	GSP								
27743	ENU11538	ANI61C6843: 25-52 2045..170	25-52	1757- 1779	GSP								
27744	ENU11539	ANI61C3259: 25-49 62..382	25-49	280-303	GSP								
27745	ENU11540	ANI61C4194: 25-50 1485..760	25-50	583-606	GSP								
27746	ENU11541	ANI61C315:3 25-51 283..2772	25-51	469-495	GSP								
27747	ENU11542	ANI61C6591: 25-54 1148..2018	25-54	771-795	GSP								

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27769	ENU11564	ANI61C5638: 3310..2406	25-48	774-798	GSP								
27770	ENU11565	ANI61C6174: 219..701	25-55	439-465	GSP								
27771	ENU11566	ANI61C1060 3:2742..1457	25-48	657-681	GSP								
27772	ENU11567	ANI61C7715: 504..163	25-52	297-324	GSP								
27773	ENU11568	ANI61C1129 4:31..565	25-48	467-489	GSP								
27774	ENU11569	ANI61C2468: 2924..3410	25-52	445-468	GSP								
27775	ENU11570	ANI61C1135: 3418..4128	25-49	362-390	GSP								
27776	ENU11571	ANI61C1010 7:1958..970	25-48	858-888	GSP								
27777	ENU11572	ANI61C8881: 3578..2998	25-44	482-507	GSP								
27778	ENU11573	ANI61C7430: 3283..2845	25-45	352-375	GSP								
27779	ENU11574	ANI61S3448: 395..218	25-48	422-447	GSP								
27780	ENU11575	ANI61C1044 4:1424..1025	25-43	357-384	GSP								
27781	ENU11576	ANI61C4788: 36..1751	25-52	1615-1644	GSP								
27782	ENU11577	ANI61C8293: 1673..986	25-42	274-294	GSP								
27783	ENU11578	ANI61C9179: 8464..8698	25-45	212-231	GSP								
27784	ENU11579	ANI61C7782: 8..383	25-48	360-381	GSP								
27785	ENU11580	ANI61C932:2 006..3728	25-51	1629-1662	GSP								

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27788	ENU11583	ANI61C8766: 107..2613	25-51	1412-1434	GSP								
27789	ENU11584	ANI61C5133: 2120..1014	25-51	1046-1065	GSP								
27790	ENU11585	ANI61C6550: 387..49	25-45	298-321	GSP								
27791	ENU11586	ANI61C5101: 1466..1044	25-47	377-405	GSP								
27792	ENU11587	ANI61C5399: 2833..3440	25-50	537-561	GSP								
27793	ENU11588	ANI61C6236: 498..136	25-52	314-345	GSP								
27794	ENU11589	ANI61C9357: 3491..2136	25-46	1158-1176	GSP								
27795	ENU11590	ANI61C2979: 488..177	25-48	270-294	GSP								
27796	ENU11591	ANI61C1030 2:6383..6825	25-54	398-426	GSP								
27797	ENU11592	ANI61C1209: 10967..12733	25-47	1045-1068	GSP								
27798	ENU11593	ANI61C8694: 2055..3109	25-48	748-771	GSP								
27799	ENU11594	ANI61S2333: 355..8	25-44	299-330	GSP								
27800	ENU11595	ANI61C9231: 292..1474	25-52	1013-1041	GSP								
27801	ENU11596	ANI61C1082 4:1361..5	25-55	1255-1284	GSP								
27802	ENU11597	ANI61C8728: 339..2251	25-52	1711-1734	GSP								
27803	ENU11598	ANI61C7107: 382..1841	25-52	1278-1299	GSP								
27804	ENU11599	ANI61C2617: 100..337	25-52	216-240	GSP								

Gene Ontology

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27807	ENU11602	ANI61C1093 1:738..214	25-47	473-507	GSP								
27808	ENU11603	ANI61C7422: 25-53 2571..2159	25-53	583-606	GSP								
27809	ENU11604	ANI61C6595: 25-46 5436..5909	25-46	432-456	GSP								
27810	ENU11605	ANI61C9031: 25-44 983..1370	25-44	285-309	GSP								
27811	ENU11606	ANI61C8413: 25-43 1182..426	25-43	664-687	GSP								
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27813	ENU11608	ANI61C7049: 25-47 1571..452	25-47	954-975	GSP								
27814	ENU11609	ANI61C8615: 25-49 2586..2137	25-49	409-432	GSP								
27815	ENU11610	ANI61C4383: 25-48 1287..1505	25-48	177-201	GSP								
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27818	ENU11613	ANI61C6429: 25-46 8288..7822	25-46	334-357	GSP								
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27821	ENU11616	ANI61C2236: 25-49 2045..3023	25-49	893-915	GSP								
27822	ENU11617	ANI61C4676: 25-49 136..375	25-49	189-222	GSP								
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27845	ENU11640	ANI61C723:1 25-52 160..2623	25-52	1038-1065	GSP								
27846	ENU11641	ANI61C3056: 25-51 2662..348	25-51	1262-1287	GSP								
27847	ENU11642	ANI61C4797: 25-48 3792..2825	25-48	802-834	GSP								
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27852	ENU11647	ANI61C7999: 25-52 3808..1181	25-52	1179-1206	GSP								
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27854	ENU11649	ANI61C8379: 25-46 2450..1302	25-46	1064-1083	GSP								
27855	ENU11650	ANI61C3792: 25-50 649..2147	25-50	842-870	GSP								
27856	ENU11651	ANI61C8900: 25-49 1873..3008	25-49	755-783	GSP								
27857	ENU11652	ANI61C1060 25-53 4:2227..993	25-53	1076-1110	GSP								
27858	ENU11653	ANI61C900:2 25-53 5..2170	25-53	950-972	GSP								
27859	ENU11654	ANI61C1158: 25-44 7256..8420	25-44	887-912	GSP								
27860	ENU11655	ANI61C6523: 25-56 71..2129	25-56	1207-1233	GSP								
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27862	ENU11657	ANI61C6977: 1669..735	25-52	849-876	GSP								
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27864	ENU11659	ANI61C6235: 1607..3436	25-42	1636-1662	GSP								
27865	ENU11660	ANI61C2443: 1157..1	25-50	774-801	GSP								
27866	ENU11661	ANI61C6248: 10252..9321	25-45	843-864	GSP								
27867	ENU11662	ANI61C1005: 5:3484..1762	25-45	1427-1458	GSP								
27868	ENU11663	ANI61C1046: 1:4279..2095	25-52	756-786	GSP								
27869	ENU11664	ANI61C6909: 1098..2118	25-56	1013-1038	GSP								
27870	ENU11665	ANI61C9006: 5050..6295	25-42	844-861	GSP								
27871	ENU11666	ANI61C5479: 1192..2303	25-49	973-996	GSP								
27872	ENU11667	ANI61C7941: 920..25	25-48	788-810	GSP								
27873	ENU11668	ANI61C7036: 846..1	25-52	1005-1032	GSP								
27874	ENU11669	ANI61C1160: 10913..12870	25-46	1460-1485	GSP								
27875	ENU11670	ANI61C1103: 8:2508..4082	25-49	864-888	GSP								
27876	ENU11671	ANI61C1103: 8:2508..4082	25-47	1035-1059	GSP								
27877	ENU11672	ANI61C6868: 3541..3697	25-49	776-810	GSP								
27878	ENU11673	ANI61C3839: 1495..74	25-47	1230-1248	GSP								
27879	ENU11674	ANI61C317:3 567..4711	25-48	874-897	GSP								
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27903	ENU11698	ANI61C8876: 25-49 1031..2327	25-49	1119-1149	GSP								
27904	ENU11699	ANI61C6064: 25-42 2164..4140	25-42	919-942	GSP								
27905	ENU11700	ANI61C6256: 25-48 5207..4223	25-48	834-858	GSP								
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27909	ENU11704		48-71	754-779	CDS	U34740							
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27911	ENU11706		37-60	750-779	CDS	AB014886							
27912	ENU11707		37-60	755-779	CDS	AF019254							
27913	ENU11708		34-57	754-779	CDS	Z68905							
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27915	ENU11710		31-54	756-779	CDS	Z68904							
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27919	ENU11714		26-49	747-779	CDS	X82827							
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27921	ENU11716		25-48	748-779	CDS	AF032987							
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27927	ENU11722		23-47	754-779	CDS	X82289							
27928	ENU11723		23-46	755-779	CDS	U34740							
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27934	ENU11729		22-51	758-779	CDS	AB000125							
27935	ENU11730		22-48	750-779	CDS	U52362							
27936	ENU11731		22-48	747-779	CDS	M58289							
27937	ENU11732		22-57	757-779	CDS	M83232							
27938	ENU11733		22-45	750-779	CDS	Y15996							
27939	ENU11734		25-42	712-729	CDS	D10019							
27940	ENU11735		25-53	712-738	CDS	X15441							
27941	ENU11736		25-48	845-867	CDS	U63728							
27942	ENU11737		25-48	1004-	CDS	Z80341							
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27943	ENU11738		25-45	1021-	CDS	AF041976							
				1038									
27944	ENU11739		25-49	1099-	CDS	U28804							
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27945	ENU11740		25-44	1257-	CDS	L41670							
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27946	ENU11741		25-44	1257-	CDS	AJ001836							
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27947	ENU11742		25-48	1321-	CDS	X15479							
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27948	ENU11743		25-50	1383-	CDS	U89675							
				1404									
27949	ENU11744		25-43	1389-	CDS	Z49834							
				1413									
27950	ENU11745		25-45	1404-	CDS	U59148							
				1425									
27951	ENU11746		25-45	1606-	CDS	M16371							
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27952	ENU11747		25-48	1643-	CDS	AF055287							
				1662									
27953	ENU11748		25-44	1991-	CDS	U21220							
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27954	ENU11749		25-46	2041-	CDS	AF027213							
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Gene Descriptions

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27957	ENU11752		25-46	300-321	CDS	M96993							
27958	ENU11753		25-45	365-390	CDS	U12632							
27959	ENU11754		25-45	377-402	CDS	X55547							
27960	ENU11755		25-46	404-429	CDS	J05545							
27961	ENU11756		25-50	418-441	CDS	X13525							
27962	ENU11757		25-50	418-441	CDS	X04696							
27963	ENU11758		25-48	443-462	CDS	U75874							
27964	ENU11759		25-49	497-525	CDS	D32070							
27965	ENU11760		25-45	573-600	CDS	Y08866							
27966	ENU11761		25-53	630-657	CDS	Z49892							
27967	ENU11762		25-51	646-672	CDS	AJ001837							
27968	ENU11763		25-47	742-762	CDS	U34740							
27969	ENU11764		25-44	758-777	CDS	U96847							
27970	ENU11765		25-48	778-804	CDS	M19132							
27971	ENU11766		25-45	945-969	CDS	X13525							
27972	ENU11767		25-44	1002-1029	CDS	M16196							
27973	ENU11768		25-44	1024-1046	CDS	Z49875							
27974	ENU11769		25-51	1031-1053	CDS	AF032988							
27975	ENU11770		25-48	1087-1107	CDS	M22869							
27976	ENU11771		25-46	1114-1135	CDS	AJ001157							
27977	ENU11772		25-44	1222-1242	CDS	AF098669							
27978	ENU11773		25-45	1258-1278	CDS	M20631							
27979	ENU11774		25-43	1270-1293	CDS	AF029318							
27980	ENU11775		25-43	1270-1293	CDS	U19394							

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28003	ENU11798		25-45	267-291		CDS	X55550							
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28043	ENU11838		25-54	1187-1218	CDS	AF043231							
28044	ENU11839		25-60	1208-1230	CDS	D87063							
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28055	ENU11850		25-50	1489-1509	CDS	Y13759							
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28058	ENU11853		25-45	1540-1566	CDS	X56671							
28059	ENU11854		25-45	1553-1581	CDS	X13525							
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28064	ENU11859		25-49	1676-1704	CDS	X82541							
28065	ENU11860		25-47	1733-1752	CDS	AJ000996							
28066	ENU11861		25-49	1729-1752	CDS	M83569							
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28072	ENU11867		25-50	2197-2226	CDS	AF043229							
28073	ENU11868		25-47	2254-2277	CDS	M31517							
28074	ENU11869		25-54	2261-2292	CDS	X64603							
28075	ENU11870		25-48	2283-2307	CDS	X99624							
28076	ENU11871		25-49	2278-2307	CDS	U56696							
28077	ENU11872		25-51	2343-2370	CDS	J04850							
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28081	ENU11876		25-48	2431-2457	CDS	X06252							
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28083	ENU11878		25-51	2550-2577	CDS	L27817							
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28086	ENU11881		25-46	2581-2610	CDS	X52491							

GenBank

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28091	ENU11886		25-44	2663-2685	CDS	M77664							
28092	ENU11887		25-45	2706-2727	CDS	D83216							
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28096	ENU11891				CDS	X65866							
28097	ENU11892				CDS	M32075							
28098	ENU11893				CDS	U86620							
28099	ENU11894				CDS	U86619							
28100	ENU11895				CDS	M35967							
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28102	ENU11897				CDS	J01390							

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28106	ENU11901				CDS	V00650							
28107	ENU11902				CDS	X06961							
28108	ENU11903				CDS	U74303							
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Gene annotation

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Table 3

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1. The first part of the paper is devoted to the study of the properties of the function $f(x)$ defined by the equation $f(x) = \sum_{n=0}^{\infty} a_n x^n$, where a_n are the coefficients of the power series.

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